

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 08:08:40 ; Search time 4374 Seconds
(without alignments)
10258.237 Million cell updates/sec

Title: US-10-658-661-1
Perfect score: 926
Sequence: 1 cccgcgcgtctctctccct.....ttgtgggtggcttgccgcctc 926

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	926	100.0	926	6	AX068095	AX068095 Sequence
2	926	100.0	926	6	AX068328	AX068328 Sequence
3	924.4	99.8	926	9	AF424702	AF424702 Homo sapi
4	922.8	99.7	1379	6	AX086014	AX086014 Sequence
5	922.8	99.7	1511	9	BC022847	BC022847 Homo sapi
6	922.8	99.7	1520	6	AX925579	AX925579 Sequence
7	922.8	99.7	1532	9	AY249859	AY249859 Homo sapi
8	921.2	99.5	1290	6	BD251829	BD251829 Phosphory
9	894.2	96.6	1161	6	CQ490667	CQ490667 Sequence
10	894.2	96.6	1161	6	CQ496502	CQ496502 Sequence
11	865.4	93.5	1092	9	AF165519	AF165519 Homo sapi
12	583.4	63.0	851	9	BC016844	BC016844 Homo sapi
13	563.2	60.8	1067	6	AX086008	AX086008 Sequence
14	560.2	60.5	1067	10	AF237619	AF237619 Mus muscu
15	555	59.9	555	6	AX068352	AX068352 Sequence
16	488	52.7	2835	6	AX747976	AX747976 Sequence
17	488	52.7	2835	9	AK093183	AK093183 Homo sapi
18	421.2	45.5	687	6	AX068347	AX068347 Sequence
19	334.4	36.1	416	6	CQ685895	CQ685895 Sequence

20	334.4	36.1	3824	6	CQ849919	CQ849919 Sequence
21	334.4	36.1	3824	9	AK128760	AK128760 Homo sapi
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24	334.4	36.1	176762	2	AC141309	AC141309 Homo sapi
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c 26	334.4	36.1	190453	2	AC139253	AC139253 Homo sapi
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28	334.4	36.1	196835	2	AC142538	AC142538 Homo sapi
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36	332.8	35.9	190078	2	AC139289	AC139289 Homo sapi
37	332.8	35.9	196715	2	AC141600	AC141600 Homo sapi
38	332.8	35.9	206252	2	AC141064	AC141064 Homo sapi
39	332.8	35.9	211552	2	AC141271	AC141271 Homo sapi
c 40	332.8	35.9	220212	2	AC141603	AC141603 Homo sapi
41	331.2	35.8	172307	2	AC044842	AC044842 Homo sapi
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c 43	320.8	34.6	238725	2	AC140828	AC140828 Homo sapi
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ALIGNMENTS

RESULT 1
AX068095
LOCUS AX068095 926 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 1 from Patent WO0102581.
ACCESSION AX068095
VERSION AX068095.1 GI:12578312
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS LucHE, R.M. and Wei, B.
TITLE Dep-3 dual-specificity phosphatase
JOURNAL Patent: WO 0102581-A 1 11-JAN-2001;
Ceptyr, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN

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Qy	61	GCTAGCTTTCGCTTCAGCCACCATGGGATGGATGGAACAAGATCTTGGCCGCTCTGT	120	
Db	61	GCTAGCTTTCGCTTTCAGCCACCATGGGATGGATGGAACAAGATCTTGGCCGCTCTGT	120	
Qy	121	ACATCGGCAACTTCAAAGATGCCAGAGACGGGAACTTGGAGCAAGCAAGGTGACAC	180	
Db	121	ACATCGGCAACTTCAAAGATGCCAGAGACGGGAACTTGGAGCAAGCAAGGTGACAC	180	
Qy	181	ATATTTCTGTCTGCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA	240	
Db	181	ATATTTCTGTCTGCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA	240	

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DB |||||||
QY 181 ATATTCTGCTGTCCACATAGTGCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
DB |||||||
QY 437 ATATTCTGCTGTCCACATAGTGCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 496
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QY 241 TCCAGACGGGATTCACATCTCAAAACCTGACAAGACATTTCAAAGAAATTAAT 300
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DB |||||||
QY 301 TCATTTCAGAGTCCGGCTCCGCGTGAGAGTCTGTTACACTGCTGCGCGGGTCT 360
DB |||||||
QY 557 TCATTTCAGAGTCCGGCTCCGCGTGAGAGTCTGTTACACTGCTGCGCGGGTCT 616
DB |||||||
QY 361 CCAGGAGCGTGACATGCTGTGATCGATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
DB |||||||
QY 617 CCAGGAGCGTGACATGCTGTGATCGATACATCATGACCGTCACTGACTTTGGCTGGGAGG 676
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QY 421 ATGCCCTGCACACCGTGTGCTGGGAGATCTGTGCGCAACCCCAACCTGGGCTTCCAGA 480
DB |||||||
QY 677 ATGCCCTGCACACCGTGTGCTGGGAGATCTGTGCGCAACCCCAACCTGGGCTTCCAGA 736
DB |||||||
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DB |||||||
QY 737 GACAGCTCCAGAGTTTCAGAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAG 796
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QY 541 AATATGAGAGAGCGCTTTGAGGATGCAAGAGCAAGCAAAACATTTCTGGCCGCTCCAG 600
DB |||||||
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DB |||||||
QY 1157 ACTGCTTGTGGTGGCTTGGCGCTC 1182
DB |||||||

RESULT 5
BC022847
LOCUS BC022847 1511 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens dual specificity phosphatase 22, mRNA (cdna clone
MGC:15090 IMAGE:3942055), complete cds.
ACCESSION BC022847
VERSION BC022847.2 GI:33872098
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1511)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Shapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Vallalath,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvachenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Duckworth,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnier,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1511)
Strausberg,R.
Direct Submission
Submitted (04-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:18605516.
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 25 Row: f Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21314693.
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DAEEAKNILAAPGLIKFWAFRLRL"
ORIGIN
Query Match 99.7%; Score 922.8; DB 9; Length 1511;
Best Local Similarity 99.8%; Pred. No. 1.6e-236;

PI GUEGLER,
PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU
YOUNG,
PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA
PI M LU,
PI LEO L SHIH
PC C12N15/09, A61K38/00, A61K45/00, A61P1/04, A61P1/16, A61P3/10 PC
, A61P5/14, A61P5/38,
PC A61P7/00, A61P9/10, A61P11/00, A61P17/00, A61P19/02, A61P19/06, PC
A61P21/04,
PC A61P25/00, A61P25/08, A61P25/14, A61P25/16, A61P25/18, A61P25/28,
PC A61P31/04,
PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P35/02,
PC A61P37/00,
PC A61P37/08, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/
PC 12, C12N9/16,
PC C1201/58, G01N33/50, G01N33/566, C12N15/00, C12N5/00, A61K37/02 CC
Incyte Clone Number: 2696537
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FT Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES
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Query Match 99.5%; Score 921.2; DB 6; Length 1290;
Best Local Similarity 99.7%; Pred. No. 4.2e-236;
Matches 923; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 215 GCTAGCGTTCGCTTCAGCCACCATGGGGAATGGATGAACAAGATCCTGCGCGCGCTGT 274
QY 121 ACATCGGCACTTCAAGATGCCAGAGCGGGAACAATTGAGCAAGAACAAAGTGACAC 180
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QY 301 TCATTCACGAGTGCCTGCGGTGAGAGTGCCTTTGATACATGCTGCGCGGGTCT 360
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QY 421 ATGCCCTGCACACCGTGCCTGGGAGATCCTGTGCCAACCCCAACCGTGGGCTTCCAGA 480
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QY 481 GACAGCTCCAGGAGTTTGAAGCATGAGGTCCATCATGATTCGGCAGTGGCTGAAGGAAG 540
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QY 841 TGCTGTGGAGTTTCTGCTACCTGCTGGATGCTGTAAGGATCCCGGGAGCCTTGGCGC 900
DB 995 TGCTGTGGAGTTTCTGCTACCTGCTGGATGCTGTAAGGATCCCGGGAGCCTTGGCGC 1054
QY 901 ACTGCCCTTGTGGGTGGCTTGGCGCTC 926
DB 1055 ACTGCCCTTGTGGGTGGCTTGGCGCTC 1080

RESULT 9
CQ490667
LOCUS 1161 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 22534 from Patent WO0160860.
ACCESSION CQ490667
VERSION CQ490667.1 GI:41456286
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 22534 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
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ORIGIN
Query Match 96.6%; Score 894.2; DB 6; Length 1161;
Best Local Similarity 99.7%; Pred. No. 7.5e-229;
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 28 GCCATAGTGCCTGCGACATGG 87
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QY 88 GGAATGGATGAACAAGATCCTGCCCGCTGTACATCGCAACTTCAAGATCCAGAG 147
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Db 727 TTTCAATTTGAAGTGAATATATACGTAGTCACTGTTTATGTTGAGAAGTAAAGGATATTTCTT 786
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RESULT 10
CQ496502 1161 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 28369 from Patent WO0160860.
ACCESSION CQ496502
VERSION CQ496502.1 GI:41462121
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Schlegel,R., Endege,W.O. and Monahan,J.E.
Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 28369 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
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ORIGIN
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Qy 28 GCCATAGTGGCCCTGCGACACACAGCGCGGGCGCTAGCGTTCGCCCTTCAGCCACCATGG 87
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Qy 388 ACATCATGACCGTCACTGACTTTGGCTGGGAGTAGCCCTGCACACCGTGGCTGCTGGGA 447
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RESULT 11
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LOCUS
DEFINITION Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX)
mRNA, complete cds.
ACCESSION AF165519
VERSION AF165519
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1092)
AUTHORS
Gu,J., Huang,Q., Yu,Y., Xu,S., Wang,Y., Han,Z., Chen,Z., Zhou,J.,
Tu,Y., Gu,W., Fu,G. and Huang,C.
Novel genes expressed in hematopoietic stem/progenitor cells from
Myelodysplastic Syndromes patient
TITLE
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1092)
AUTHORS Gu, J., Huang, Q., Yu, Y., Xu, S., Wang, Y., Han, Z. and Chen, Z.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P.R. China
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QY 900 CACTGCTTGTGGTGGCTTGGGCGTC 926
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RESULT 12
BC016844
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DEFINITION Homo sapiens dual specificity phosphatase 22, mRNA (CDNA clone
IMAGE:3905407), complete cds.
ACCESSION BC016844
VERSION BC016844.1 GI:16877148
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 851)
AUTHORS Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Sapleton, T.E., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.E., Hale, J.A., Gunaratne, P.H., Richards, S.,
Wyllie, D.K., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, K.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Pahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalish, D.E.,
Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED 12477932
REFERENCE 2 (bases 1 to 851)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 22 Row: i Column: 13
 This clone has the following problem: The cds is short compared to the longest cds in the locus.

FEATURES

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ORIGIN

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 LOCUS
 DEFINITION Sequence 5 from Patent WO0112819.
 AX086008
 VERSION AX086008.1 GI:13275835
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Plowman,G.D., Martinez,R., Whyte,D., Hill,R., Flanagan,P. and
 Lioubin,M.
 TITLE Protein phosphatases and diagnosis and treatment of
 phosphatase-related disorders
 JOURNAL Patent: WO 0112819-A 5 22-FEB-2001;
 Sugen, Inc. (US)
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RESULT 14
AF237619 1067 bp mRNA linear ROD 17-JUL-2001
LOCUS Mus musculus dual specificity phosphatase TS-DSP2 mRNA, complete
DEFINITION
ACCESSION AF237619
VERSION AF237619.1 GI:13183068
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 1067)
MEDLINE Aoyama,K., Nagata,M., Oshima,K., Matsuda,T. and Aoki,N.
PUBMED Molecular cloning and characterization of a novel dual specificity
phosphatase, LMW-DSP2, that lacks the cdc25 homology domain
J. Biol. Chem. 276 (29), 27575-27583 (2001)
21347909
11346645
REFERENCE 2 (bases 1 to 1067)
AUTHORS Aoyama,K., Matsuda,T. and Aoki,N.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2000) Applied Molecular Biosciences, Nagoya
University, Furo-cho, Chikusa-ku, Nagoya, Aichi 464-8601, Japan
FEATURES
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Best Local Similarity 85.5%; Pred. No. 4e-139;
Matches 678; Conservative 0; Mismatches 93; Indels 22; Gaps 4;
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RESULT 15
AX068352 555 bp DNA linear PAT 25-JAN-2001
LOCUS Sequence 25 from Patent WO0102582.
DEFINITION
ACCESSION AX068352
VERSION AX068352.1 GI:12578520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Luche,R.M. and Wei,B.
TITLE Dsp-3 dual-specificity phosphatase
JOURNAL Patent: WO 0102582-A 25 11-JAN-2001;
Ceptyr, Inc. (US)
FEATURES
source Location/Qualifiers
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ORIGIN

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59.9%; Score 555; DB 6; Length 555;									
Best Local Similarity 100.0%; Pred. No. 9.3e-138;									
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	84	ATGGGGAATGGGATGAACAAGATCCTGCCCCGGCCTGTACATCGGCAACTTCAAAGATGCC	143						
Db	1	ATGGGGAATGGGATGAACAAGATCCTGCCCCGGCCTGTACATCGGCAACTTCAAAGATGCC	60						
Qy	144	AGAGACGGGAAACAATTAGCAAGAAACAAGTGACACATATTTCTGTCTGTCCACGATAGT	203						
Db	61	AGAGACGGGAAACAATTAGCAAGAAACAAGTGACACATATTTCTGTCTGTCCACGATAGT	120						
Qy	204	GCCAGGCCATGTGGAGGGAGTTAAATACCTGTGTCATCCCGAGCGGATTCACCATCT	263						
Db	121	GCCAGGCCATGTGGAGGGAGTTAAATACCTGTGTCATCCCGAGCGGATTCACCATCT	180						
Qy	264	CAAAACCTGACAGACATTTCAAAGAAAGTATTAAATTCATTACGAGTGCCGGCTCCGC	323						
Db	181	CAAAACCTGACAGACATTTCAAAGAAAGTATTAAATTCATTACGAGTGCCGGCTCCGC	240						
Qy	324	GGTGAGAGCTGCCTTGTACACTGCTGGCCGGGGTCTCCAGGAGCGTGACACTGGTGATC	383						
Db	241	GGTGAGAGCTGCCTTGTACACTGCTGGCCGGGGTCTCCAGGAGCGTGACACTGGTGATC	300						
Qy	384	GCATACATCATGACCGTCACCTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGTGCT	443						
Db	301	GCATACATCATGACCGTCACCTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGTGCT	360						
Qy	444	GGGAGATCCTGTGCCAACCCCAAGCTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAG	503						
Db	361	GGGAGATCCTGTGCCAACCCCAAGCTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAG	420						
Qy	504	CATGAGTCCATCAGTATCGGCAGTGGCTGAAGGAAGAAATATGGAGAGAGCCCTTTGCAG	563						
Db	421	CATGAGTCCATCAGTATCGGCAGTGGCTGAAGGAAGAAATATGGAGAGAGCCCTTTGCAG	480						
Qy	564	GATCAGAAGAGCCAAAACATTTGGCCGCTCCAGGAATTTCTGAAGTTCTGGGCCCTTT	623						
Db	481	GATCAGAAGAGCCAAAACATTTGGCCGCTCCAGGAATTTCTGAAGTTCTGGGCCCTTT	540						
Qy	624	CTCAGAAGACTGTAA	638						
Db	541	CTCAGAAGACTGTAA	555						

Search completed: July 21, 2005, 15:47:16
Job time : 4380 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 13:21:46 ; Search time 372 Seconds
(without alignments)
4073.097 Million cell updates/sec

Title: US-10-658-661-1

Perfect score: 926

Sequence: 1 cccgcgcctctctctccct.....ttgtgggtggtggtgcgc 926

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA.*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	77.4	8.4	315	4	US-09-513-999C-16851
2	70	7.6	743	4	US-09-270-767-12522
3	62.6	6.8	1830	4	US-09-557-921-1
4	59.8	6.5	1746	4	US-09-949-016-5068
5	59.8	6.5	2473	4	US-09-949-016-623
6	58.4	6.3	2000	4	US-09-016-434-1291
7	58.4	6.3	2000	4	US-09-919-497-10
8	58.4	6.3	2015	4	US-09-949-016-4969
9	57.8	6.2	1619	4	US-09-702-705-801
10	57.8	6.2	1619	4	US-09-736-457-801
11	57.8	6.2	1619	4	US-09-614-124B-801
12	57.8	6.2	1619	4	US-09-671-325-801
13	57.8	6.2	1619	4	US-09-589-184-801
14	57.8	6.2	1619	4	US-09-658-824-801
15	57.8	6.2	2240	4	US-09-016-434-1100
16	57.8	6.2	4637	4	US-09-702-705-804
17	57.8	6.2	4637	4	US-09-736-457-804
18	57.8	6.2	4637	4	US-09-614-124B-804
19	57.8	6.2	4637	4	US-09-671-325-804
20	57.8	6.2	4637	4	US-09-589-184-804
21	57.8	6.2	4637	4	US-09-658-824-804
22	57.4	6.2	944	4	US-09-371-671B-10
23	57	6.2	950	4	US-09-799-451-935
24	57	6.2	1212	4	US-09-976-594-663
25	56.2	6.1	1238	2	US-08-530-290-11
26	56.2	6.1	1238	4	US-09-702-705-803
27	56.2	6.1	1238	4	US-09-736-457-803

28	56.2	6.1	1238	4	US-09-614-124B-803	Sequence 803, App
29	56.2	6.1	1238	4	US-09-671-325-803	Sequence 803, App
30	56.2	6.1	1238	4	US-09-589-184-803	Sequence 803, App
31	56.2	6.1	1238	4	US-09-658-824-803	Sequence 803, App
32	56.2	6.1	1987	2	US-08-990-379-1	Sequence 1, Appli
33	56.2	6.1	1993	2	US-08-990-379-2	Sequence 2, Appli
34	56.2	6.1	2064	4	US-09-702-705-825	Sequence 825, App
35	56.2	6.1	2064	4	US-09-736-457-825	Sequence 825, App
36	56.2	6.1	2064	4	US-09-614-124B-825	Sequence 825, App
37	56.2	6.1	2064	4	US-09-671-325-825	Sequence 825, App
38	56.2	6.1	2064	4	US-09-589-184-825	Sequence 825, App
39	56.2	6.1	2064	4	US-09-658-824-825	Sequence 825, App
40	56.2	6.1	2109	4	US-09-702-705-826	Sequence 826, App
41	56.2	6.1	2109	4	US-09-736-457-826	Sequence 826, App
42	56.2	6.1	2109	4	US-09-614-124B-826	Sequence 826, App
43	56.2	6.1	2109	4	US-09-671-325-826	Sequence 826, App
44	56.2	6.1	2109	4	US-09-589-184-826	Sequence 826, App
45	56.2	6.1	2109	4	US-09-658-824-826	Sequence 826, App

ALIGNMENTS

RESULT 1
US-09-513-999C-16851/c
; Sequence 16851, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16851
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16851

Query Match	8.4%	Score	77.4	DB	4	Length	315
Best Local Similarity	88.4%	Pred. No.	1.4e-13				
Matches	84	Conservative	0	Mismatches	11	Indels	0
Gaps	0						
Qy	24	ACATGCCATAGTGCCTGCGACACACACGCGCGCGCTTCCCTTCAGCCACC	83				
Db	162	ACATGCCATAGTGCCTGCGACACACACGCGCGCGCTTCCCTTCAGCCACC	103				
Qy	84	ATGGGGAATGGGATGAACAAGATCCTGCGCGCCT 118					
Db	102	ATGGGGAATGGGATGAACAAGATCCTGCGCCT 68					

RESULT 2
US-09-270-767-12522
; Sequence 12522, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12522
; LENGTH: 743

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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12522

Query Match          7.6%; Score 70; DB 4; Length 743;
Best Local Similarity 49.8%; Pred. No. 4.6e-11;
Matches 212; Conservative 0; Mismatches 205; Indels 9; Gaps 1;

Qy 97 TGAACAAGATCCTGCCCGCTGTACATCGGCAACTTCAAAAGATGCCAGAGACGCGGAAC 156
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
37 TGGAGATAATCCCTGGACTACTCTCTCTCGGGAATGCCACACAGCTGGCACTCGGAAG 96
Qy 157 AATTGAGCAAGACAGAGTGACATATTCTGTCTCCAGATAGTGCAGGCTATGT 216
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 CGTTGAAAAGTACAATATAAAGTATGTTTGAATGTGACACCAAGATTGGCAAAATAGT 156
Qy 217 T-----GGAGGAGTAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCAA 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 TCAAGGAGTCGGGACATCAAGTATCTGCAGATTCGATCAGGATCACTACTACAAA 216
Qy 268 ACCTGACAAGACATTTCAAAGAAAGTATTAATTCATTACAGAGTCCGGCTCCGCGTG 327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 ATTTGGCCATACATTTCCCGGATGCCATACAGTTTATAGAGAAAGCGGTCCGCAAGCT 276
Qy 328 AGAGTGCCTTGTACATGCTGCCGGGGTCTCCAGAGCGTGACACTGTGTATCGCAT 387
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
277 CGGTGGTGTCTGTCTCACTGCTGCCGGAGTTTCGCGCTCGGTGACCGTGACGCTCGCT 336
Qy 388 ACATCATGACCGCTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGGGA 447
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 ACTTGATGCACACGGGGGCTGAGTCTCAACGAGCGCTTCGCGATGTTGCGGACCGGA 396
Qy 448 GATCCTGTGCCAACCCCAACGTCGGCTTCAGAGACAGCTCCAGGAGTTTGAGAAAGCATG 507
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
397 AGCCGGATGTATCGCCCAACTTCCACTTTCATGTCGAGCAGCTGCTCTCTCTCGAGACCAAC 456
Qy 508 AGGTCC 513
Db |||||
457 TGCGCC 462

RESULT 3
US-09-557-921-1
; Sequence 1, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Lucie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-921-1

Query Match          6.8%; Score 62.6; DB 4; Length 1830;
Best Local Similarity 51.6%; Pred. No. 1.5e-08;
Matches 143; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

Qy 226 TTAATACCTGTGATCCAGCAGCGGATTCACCATCTCAAACCTGACAAAGACATTCA 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1189 TCACTACAGCGGTGCCGCCACTGACAGCAACAGCAACTGCGGAGTACTTTG 1248
Qy 286 AAGAAAGTATTAATTCATTACAGAGTCCGGCTCCGGGTGAGAGCTGCTGTATCACT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1249 AAGAGGCTTTTGAAGTATTGAGGAAGCTACACAGTGTGGGAAGGGGCTTCTCATCCACT 1308
Qy 346 GCCTGGCCGGGTCTCCAGGAGCGTGACACTGGTGTGATCGCATACATGACCGTCACTG 405
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Db 1309 GCCAGGCTGGGGTGTCCCGCTCCGCCACCATCGTCTACTCGTATGATGAAGCACACTC 1368
Qy 406 ACTTTGGCTGGAGGATGCCCTGCACACCGCTGCTGGGAGATCCTGTGCCCAACCCCA 465
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1369 GGATGACCATGACTGATGCTTATAAATTTGTCAAAGGCAACGACCAATATCTCTCCCA 1428
Qy 466 ACCTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAA 502
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1429 ACCTTAACCTTCATGGGGCAGTTGCTAGAGTTGAGGA 1465

RESULT 4
US-09-949-016-5068
; Sequence 5068, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5068
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5068

Query Match          6.5%; Score 59.8; DB 4; Length 1746;
Best Local Similarity 51.3%; Pred. No. 1.1e-07;
Matches 139; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 229 AATACCTGTGCATCCAGCAGCGGATTCACCATCTCAAACCTGACAAAGACATTTCAAG 288
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 ACTACAATAGATCCCTGTGTGGAAGACAGCCACGCGTGACATTAGTCCCACTTTCAAG 210
Qy 289 AAAGTATTAATTCATTACAGAGTGCGCGCTCCCGGTGAGAGCTGCTGTGTACACTGCC 348
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 AAGCATAGACTTCATTGACTGTGTGAGGAAAGGAGGCAAGGTCTGTGTCACCTGTG 270
Qy 349 TGCCCGGGGTCTCCAGGAGCGTGACACTGGTGTATCGCATATCATCATCGCTCACTGACT 408
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
271 AGGCTGGGATCTCCCGTTACCCCAACCATCTGCATGGCTTACCTTATGAAGACCAAGCAGT 330
Qy 409 TTGCTGGGAGGATGCCCTGCACACCGCTGCTGGGAGATCCTGTGCCAACCCCAACG 468
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 TCCGCTTGAAGGAGGCGCTTCGATTACATCAAGCAGAGGAGCATGGTCTCGCCCCAAT 390
Qy 469 TGGGCTTCCAGAGACAGCTCCAGGAGTTTGA 499
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
391 TTGGCTTATGGGCCAGCTCTCGCATACGA 421

RESULT 5
US-09-949-016-623
; Sequence 623, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 623
 ; LENGTH: 2473
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-623

Query Match 6.5%; Score 59.8; DB 4; Length 2473;
 Best Local Similarity 51.3%; Pred. No. 1.3e-07;
 Matches 139; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
 Qy 229 AATACCTGTGTCATCCACAGCGGATTCCACCATCTCAAAACCTGACAAAGACATTTCAAAG 288
 Db 881 ACTCAAAATGATCCCTGTGGAAGACAGCCACACGGCTGACATTAGCTCCCACTTTCAAG 940
 Qy 289 AAAGTATTAAATTCATTCACAGAGTCGGCTCCGGGTGAGAGCTGCTTTGTACACTGCC 348
 Db 941 AAGCAATAGACTTCAATGACTGTGTGTCAGGGAAGAGGCAAGGTCTCTGTCCACTGTG 1000
 Qy 349 TGGCGGGGTCTCCAGGAGGTGACACTGTGATCGCATACATCATGACCGTCACTGACT 408
 Db 1001 AGGCTGGGATCTCCCGTTTCAACCCACCATCTGATGGCTTACCTTATGAAGACCAAGCAGT 1060
 Qy 409 TTGGCTGGAGGATGCCCTGCACACCGTGCCTGTGTTGGGAGATCCTGTGTCACCAACCCCAACG 468
 Db 1061 TCCGCTGAAGAGGCTCTCGATTACATCAAGACAGAGGAGGATGCTCTCGCCCACT 1120
 Qy 469 TGGGCTCCAGAGACAGCTCAGAGTTGA 499
 Db 1121 TTGGCTTCATGGCCAGCTCCTGCAGTACGA 1151

RESULT 6
 US-09-016-434-1291
 ; Sequence 1291, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1291:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2000 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: G29980
 ; US-09-016-434-1291

Query Match 6.3%; Score 58.4; DB 4; Length 2000;
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
 Qy 197 CGATAGTCCAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTC 256
 Db 857 CAATTGTCCCAACCATTTTGAGGGTCACTACCACTACAAGAGCATCCCTGTGGAGGACAA 916
 Qy 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316
 Db 917 CCACAGGCGAGACATCAGCTCCTGGTTCAACGAGGCCATTGACTTCATAGACTCCATCAA 976
 Qy 317 GCTCCGGGTGAGAGCTGCTTGTACACTGCTGCGGGGTCTCCAGGAGCGTGACACT 376
 Db 977 GAATGCTGGAGGAGGGTGTGTTGTCACCTGCGAGGAGGCAATTTCCCGGTGAGCCACCAT 1036
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436
 Db 1037 CTGCTTGTCTTACCTTATGAGGACTAATCGAGTCAAGCTGGACGAGGCTTTGAGTTGT 1096
 Qy 437 GCGTGTGGGAGATCTGTGCGCAACCCCAAGTGGGCTTCCAGAGACAGCTCCAGGAGTT 496
 Db 1097 GAAGCAGAGCGAGCATCATCTCTCCCAACTTCAGCTTCATGGGCCAGCTGCTGCAGTT 1156
 Qy 497 TGAGAGCATGAGGTCCATCAGTA 520
 Db 1157 TGAGTCCAGGTGCTGGCTCGCA 1180

RESULT 7
 US-09-919-497-10
 ; Sequence 10, Application US/09919497
 ; Patent No. 6773883
 ; GENERAL INFORMATION:
 ; APPLICANT: Mutter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/7225
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/221,735
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-919-497-10

Query Match 6.3%; Score 58.4; DB 4; Length 2000;
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
 Qy 197 CGATAGTCCAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTC 256
 Db 857 CAATTGTCCCAACCATTTTGAGGGTCACTACCACTACAAGAGCATCCCTGTGGAGGACAA 916
 Qy 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316

Db 917 CCACAGGCGACATCAGCTCCTGGTTCAACAGAGGCCATTGACTTCATAGACTCCATCAA 976
 Qy 317 GCTCGCGGTGAGAGTGCCTTTGACATGCTGCTGGCGGGGTCTCCAGAGCGTGACACT 376
 Db 977 GAATGCTGGAGGAAGGGTGTGTGCTCACTGCGCAGGAGCATTTCCCGGTGAGCCACCAT 1036
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436
 Db 1037 CTGCGCTTGCCTTACCTTATGAGGACTAATCGAGTCAAGCTGACGAGGCTTTGAGTTGT 1096
 Qy 437 GCGTGTGGGAGATCCTGTGCCAACCCCAAGCTGGCTTCCAGAGACAGCTCCAGGAGTT 496
 Db 1097 GAAGCAGAGGCGAAGCATCATCTCTCCCACTTCAGCTTCATGGCCAGCTGCTGCAGTT 1156
 Qy 497 TGAGAGCATGAGTCCATCAGTA 520
 Db 1157 TGAGTCCCAAGTGTGGCTCCGCA 1180

RESULT 8
 US-09-949-016-4969
 ; Sequence 4969, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4969
 ; LENGTH: 2015
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-4969

Query Match 6.3%; Score 58.4; DB 4; Length 2015;
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
 Qy 197 CGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 256
 Db 872 CAATGTCCCAACCACTTTGAGGGTCACTACAGTACAAGAGCATCCCTGTGGAGGACAA 931
 Qy 257 ACCATCTCAAAACCTGACAGACATTTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316
 Db 932 CCACAGGCGACATCAGCTCCTGGTTCAAGAGGCCATTGACTTCATAGACTCCATCAA 991
 Qy 317 GCTCGCGGTGAGAGTGCCTTTGACATGCTGCTGGCGGGGTCTCCAGAGCGTGACACT 376
 Db 992 GAATGCTGGAGGAAGGGTGTGTGCTCACTGCGCAGGAGCATTTCCCGGTGAGCCACCAT 1051
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436
 Db 1052 CTGCGCTTGCCTTACCTTATGAGGACTAATCGAGTCAAGCTGACGAGGCTTTGAGTTGT 1111
 Qy 437 GCGTGTGGGAGATCCTGTGCCAACCCCAAGCTGGGCTTCCAGAGACAGCTCCAGGAGTT 496
 Db 1112 GAAGCAGAGGCGAAGCATCATCTCTCCCACTTCAGCTTCATGGCCAGCTGCTGCAGTT 1171
 Qy 497 TGAGAGCATGAGTCCATCAGTA 520
 Db 1172 TGAGTCCCAAGTGTGGCTCCGCA 1195

RESULT 9
 US-09-702-705-801
 ; Sequence 801, Application US/09702705
 ; Patent No. 6504010
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C14
 ; CURRENT APPLICATION NUMBER: US/09/702,705
 ; CURRENT FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 1833
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 801
 ; LENGTH: 1619
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-702-705-801

Query Match 6.2%; Score 57.8; DB 4; Length 1619;
 Best Local Similarity 50.2%; Pred. No. 4.2e-07;
 Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
 Qy 227 TAAATACCTGTGATCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 286
 Db 445 TCAGTACAGTGCATCCAGTGGGAAGATAACCAAGCGGCAGATCATCAGCTCTGGTTCA 504
 Qy 287 AGAAGTATTAAATTCATTACAGAGTCCCGGCTCCCGGTGAGAGTCCCTTGACACTG 346
 Db 505 GGAAGCCATAGATACATCATGATCCGTTGAAGGACTGCCGTGGGCGCGTCTGGTGCACTG 564
 Qy 347 CCTGGCCGGGGTCTCCAGGAGCGTGACATCTGGTGTATCGCATATCATGACCGTCACTGA 406
 Db 565 CCAGGGGGCATCTCGCGGTCCGCCACCATCTGCTGCTACCTGATGATGAAGAAACG 624
 Qy 407 CTTTGGCTGGAGGATGCTTGCACACCGTGGCTGCTGGGAGATCTCTGTGCCAACCCCAA 466
 Db 625 GGTGAGGCTGGAGGAGGCTTCGAGTTCTGTAAGCAGCGCCGAGCATTTATCTCGCCAA 684
 Qy 467 CGTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCATGAGGT 511
 Db 685 CTTGAGCTTTCATGGGGAGCTGTCAGTTCGAGTCCAGGTGCT 729

RESULT 10
 US-09-736-457-801
 ; Sequence 801, Application US/09736457
 ; Patent No. 6509448
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Lodes, Michael A.
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Vedvick, Tom
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Retter, Marc
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Wang, Aijun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C15
 ; CURRENT APPLICATION NUMBER: US/09/736,457
 ; CURRENT FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 1864

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
; ORGANISM: Homo sapien
US-09-736-457-801

Query Match      6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGGAGATTAACCAAGGCCGACATCAGCTCCTGGTTTCA 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCCGGGTGAGAGCTCCCTGTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATACATCGATCGCGTGGAGACTGCGTGGGGCGGTGGTGCACTG 564
Qy 347 CCTGGCGGGTCTCCAGAGCGTGCACACTGGTATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGGGTCCGCCACCATCTGCTGSCCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTGTTAAGCAGCGCCGACGATTTATCTCGCCCA 684
Qy 467 CGTGGCTTCCAGAGACGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTTCGAGTCCAGGTGCT 729

RESULT 11
US-09-614-124B-801
; Sequence 801, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614.124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-801

Query Match      6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGGAGATTAACCAAGGCCGACATCAGCTCCTGGTTTCA 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCCGGGTGAGAGCTCCCTGTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATACATCGATCGCGTGGAGACTGCGTGGGGCGGTGGTGCACTG 564
Qy 347 CCTGGCGGGTCTCCAGAGCGTGCACACTGGTATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGGGTCCGCCACCATCTGCTGSCCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTGTTAAGCAGCGCCGACGATTTATCTCGCCCA 684
Qy 467 CGTGGCTTCCAGAGACGCTCCAGGAGTTTGAGAGCATGAGCT 511
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Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTGTTAAGCAGCGCCGACGATTTATCTCGCCCA 684
Qy 467 CGTGGCTTCCAGAGACGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTTCGAGTCCAGGTGCT 729

RESULT 12
US-09-671-325-801
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671.325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-801

Query Match      6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGGAGATTAACCAAGGCCGACATCAGCTCCTGGTTTCA 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCCGGGTGAGAGCTCCCTGTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATACATCGATCGCGTGGAGACTGCGTGGGGCGGTGGTGCACTG 564
Qy 347 CCTGGCGGGTCTCCAGAGCGTGCACACTGGTATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTGTTAAGCAGCGCCGACGATTTATCTCGCCCA 684
Qy 467 CGTGGCTTCCAGAGACGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTTCGAGTCCAGGTGCT 729

RESULT 13
US-09-589-184-801
; Sequence 801, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick

```

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; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-801

Query Match 6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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685 CTTGAGCTTTCATGGGCGAGCTGCTGCGAGTTTCGAGTCCAGGTGCT 729

RESULT 15
US-09-016-434-1100
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1255784
; US-09-016-434-1100

Query Match 6.2%; Score 57.8; DB 4; Length 2240;
Best Local Similarity 50.2%; Pred. No. 5.1e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 227 TAAATACCTGTGCATCCAGCAGCGGATTCCACCATCTCAAACCTGACAAGACATTTCAA 286
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445 TCAGTACAAGTGATCCAGTGGAGATACCAAGCCGACATCAGCTCCTGGTTTCAT 504
QY 287 AGAAAGTATTAAATTCATTACAGAGTCCCGGCTCCGGGTGAGAGCTGCCTTTGACACTG 346
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QY 347 CCTGGCCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGA 406
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625 GGTGAGGCTGGAGGAGCCTTCGAGTTCTGTTAAGCAGCGCGGAGCATTTATCTGCCCAA 684
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685 CTTGAGCTTTCATGGGCGAGCTGCTGCGAGTTTCGAGTCCAGGTGCT 729

RESULT 14
US-09-658-824-801
; Sequence 801, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-801

Query Match 6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 227 TAAATACCTGTGCATCCAGCAGCGGATTCCACCATCTCAAACCTGACAAGACATTTCAA 286
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347	CCTGGCCGGGGTCTCCAGGAGCGTGACACT	TGGTCAATCGCATACATCATGACCCGTCACTGA	406	
959	CCAGCCGGGCATCTCGCGGTGGGCCCATCT	TGCTGGCTGACCTGATGATGAAGAAACG	1018	
407	CTTTGGCTGGAGGATGCCCTGACACCGCTG	CTGTGGAGATCTGTGTCACACCCCAA	466	
1019	GGTGAGGCTGGAGGAGGCTTCGAGTTCGTT	AACAGCGCCGACGATCATCTCGCCCAA	1078	
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Job time : 373 secs

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OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

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SUMMARIES

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2	926	100.0	926	18	US-10-444-795B-778
3	924	99.8	1187	14	US-10-103-313-239
4	923.6	99.7	1187	17	US-10-264-237-1406
5	922.8	99.7	1520	15	US-10-287-806-1
6	894.2	96.6	1161	20	US-10-357-930-22534
7	894.2	96.6	1161	20	US-10-357-930-28369

8	875.8	94.6	910	14	US-10-103-313-111	Sequence 111, Appl
9	589.4	63.7	1218	21	US-10-803-738-1	Sequence 1, Appli
10	553.4	59.8	555	15	US-10-287-806-3	Sequence 3, Appli
11	488	52.7	2835	17	US-10-104-047-1501	Sequence 1501, Ap
12	418.6	45.2	3010	21	US-10-803-738-3	Sequence 3, Appli
13	375.4	40.5	2420	15	US-10-101-510-481	Sequence 481, App
14	334.4	36.1	416	17	US-10-342-535A-30821	Sequence 30821, A
15	334.4	36.1	416	18	US-10-085-783A-30821	Sequence 30821, A
16	274.2	29.6	556	16	US-10-029-386-9710	Sequence 9710, Ap
17	270.4	29.2	279	9	US-09-294-093B-291	Sequence 291, App
18	269	29.0	277	20	US-10-425-115-150546	Sequence 150546
19	200.8	21.7	867	9	US-09-963-204-13	Sequence 13, Appli
20	200.8	21.7	867	14	US-10-151-320-41	Sequence 41, Appl
21	200.8	21.7	1160	9	US-09-963-204-1	Sequence 1, Appli
22	200.8	21.7	1160	14	US-10-151-320-42	Sequence 42, Appl
23	199.2	21.5	833	14	US-10-151-320-13	Sequence 13, Appl
24	199.2	21.5	833	18	US-10-444-795B-782	Sequence 782, App
25	199.2	21.5	1325	18	US-10-343-357-20	Sequence 20, Appl
26	199.2	21.5	1326	14	US-10-151-320-39	Sequence 39, Appl
27	199.2	21.5	1326	18	US-10-168-506-8	Sequence 8, Appli
28	199.2	21.5	1326	21	US-10-838-181-8	Sequence 8, Appli
29	198.2	21.4	705	9	US-09-963-204-3	Sequence 3, Appli
30	198.2	21.4	705	14	US-10-151-320-40	Sequence 40, Appl
31	197.6	21.3	1123	18	US-10-072-012-107	Sequence 107, App
32	180.8	19.5	1045	14	US-10-151-320-7	Sequence 7, Appli
33	180.8	19.5	1045	18	US-10-444-795B-836	Sequence 836, App
34	180.8	19.5	1064	14	US-10-151-320-11	Sequence 11, Appl
35	180.8	19.5	1064	18	US-10-444-795B-840	Sequence 840, App
36	180.8	19.5	1268	14	US-10-151-320-5	Sequence 5, Appli
37	180.8	19.5	1268	18	US-10-444-795B-834	Sequence 834, App
38	180.8	19.5	1666	14	US-10-151-320-1	Sequence 1, Appli
39	180.8	19.5	1666	18	US-10-444-795B-830	Sequence 830, App
40	180.8	19.5	1807	14	US-10-151-320-3	Sequence 3, Appli
41	180.8	19.5	1807	18	US-10-444-795B-832	Sequence 832, App
42	176	19.0	982	14	US-10-151-320-9	Sequence 9, Appli
43	176	19.0	982	18	US-10-444-795B-838	Sequence 838, App
44	173.8	18.8	567	16	US-10-029-386-13034	Sequence 13034, A
45	163.4	17.6	166	16	US-10-029-386-26734	Sequence 26734, A

ALIGNMENTS

RESULT 1
US-10-151-320-34
; Sequence 34, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Lucie, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436
; CURRENT APPLICATION NUMBER: US/10/151.320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-151-320-34

Query Match 100.0%; Score 926; DB 14; Length 926;
Best Local Similarity 100.0%; Pred. No. 7.2e-278;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCCGCGCTCCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACACACACGCGCGGC 60
Db	1	CCCCGCGCTCCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACACACGCGCGGC 60
Qy	61	GCTAGCGTTGCGCTTTCAGCCACCATGGGAATGGATGAACAAGATCTGCCCGCCTGT 120
Db	61	GCTAGCGTTGCGCTTTCAGCCACCATGGGAATGGATGAACAAGATCTGCCCGCCTGT 120


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RESULT 3
US-10-103-313-239/c
; Sequence 239, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 239
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-239

Query Match          99.8%; Score 924; DB 14; Length 1187;
Best Local Similarity 99.8%; Pred. No. 3.5e-277;
Matches 924; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGCGCTCTCTCTCTTAACATGCCATAGTGGCCCTGGACACACACGCGCGGGC 60
Db 1156 CCCGCGCTCTCTCTCTTAACATGCCATAGTGGCCCTGGACACACACGCGCGGGC 1097

Qy 61 GCTAGCGTTCCGCTTCAGCCACCATGGGAATGGATGAAACAAGATCTGCGCGGCTGT 120
Db 1096 GCTAGCGTTCCGCTTCAGCCACCATGGGAATGGATGAAACAAGATCTGCGCGGCTGT 1037

Qy 121 ACATCGGCACTTCAAGATGCGAGACGCGGAACCAATTCAGCAAGAAACAAGGTGACAC 180
Db 1036 ACATCGGCACTTCAAGATGCGAGACGCGGAACCAATTCAGCAAGAAACAAGGTGACAC 977

Qy 181 ATATTCTGTCTGTCCACGATAGTCCAGGCTCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
Db 976 ATATTCTGTCTGTCCACGATAGTCCAGGCTCTATGTTGGAGGGAGTTAAATACCTGTGCA 917

Qy 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTATTAAT 300
Db 916 TCCAGAGCGGATTCACCATCTCAAAACCTGACAAAGACATTTCAAGAAAGATTATTAAT 857

Qy 301 TCATTTCAGAGTGGCGGCTCCGCGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCT 360
Db 856 TCATTTCAGAGTGGCGGCTCCGCGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCT 797

Qy 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 796 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 737

Qy 421 ATGCCCTGCACACGCTGCTGGGAGATCTGTGCCAACCCCAACGTTGGGCTTCCAGA 480
Db 736 ATGCCCTGCACACGCTGCTGGGAGATCTGTGCCAACCCCAACGTTGGGCTTCCAGA 677

Qy 481 GACAGCTCCAGAGTTTCAGAAAGCATGAGTCCATCAGTATCGGCAGTGGCTGAAGGAAG 540
Db 676 GACAGCTCCAGAGTTTCAGAAAGCATGAGTCCATCAGTATCGGCAGTGGCTGAAGGAAG 617

Qy 541 AATATGGAGAGAGCCCTTTTGAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 616 AATATGGAGAGAGCCCTTTTGAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 557

Qy 601 GAAATTCGAAGTTCTGGGCTTTCTCAGAAAGCTGTAATGATACCTGAAGTTTCTGAATA 660
Db 556 GAAATTCGAAGTTCTGGGCTTTCTCAGAAAGCTGTAATGATACCTGAAGTTTCTGAATA 497

Qy 661 TTGAAACCCGACAGTTTTCAGGCTGCTCCAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 496 TTGAAACCCGACAGTTTTCAGGCTGCTCCAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 437

Qy 721 TATCCAGTAGTGAATTTGTAACCTTGTGTTTTCATTGTAAGCTGAATATATATACGTAGTCATG 780

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Db 436 TATCCAGTAGTGAATTTGTAACCTTGTGTTTTCATTGTAAGCTGAATATATACGTAGTCATG 377
Qy 781 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 840
Db 376 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 317
Qy 841 TGCTGTGGAGGTTTCTGTACTCTGCTTGGATGCCCTGTAAGGATCCCGGAGCCTTGGCGC 900
Db 316 TGCTGTGGAGGTTTCTGTACTCTGCTTGGATGCCCTGTAAGGATCCCGGAGCCTTGGCGC 257
Qy 901 ACTGCTTGGGTTGGCTTGGCGCTC 926
Db 256 ACTGCTTGGGTTGGCTTGGCGCTC 231

RESULT 4
US-10-264-237-1406
; Sequence 1406, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1406
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1406

Query Match          99.7%; Score 923.6; DB 17; Length 1187;
Best Local Similarity 99.7%; Pred. No. 4.7e-277;
Matches 923; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGCGCTCTCTCTCTCTGTAACATGCCATAGTGGCCCTGGACACACACGCGCGGGC 60
Db 32 CCCGCGCTCTCTCTCTCTGTAACATGCCATAGTGGCCCTGGACACACACGCGCGGGC 91

Qy 61 GCTAGCGTTGCGCTTCAGCCACCATGGGAAATGGGATGAAACAAGATCTGCGCGGCTGT 120
Db 92 GCTAGCGTTGCGCTTCAGCCACCATGGGAAATGGGATGAAACAAGATCTGCGCGGCTGT 151

Qy 121 ACATCGGCACTTCAAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGGTGACAC 180
Db 152 ACATCGGCACTTCAAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGGTGACAC 211

Qy 181 ATATTCTGTCTGTCCACGATAGTGGCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
Db 212 ATATTCTGTCTGTCCACGATAGTGGCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 271

Qy 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACACACATTTTCAAGAAAGATTATTAAT 300
Db 272 TCCAGAGCGGATTCACCATCTCAAAACCTGACACACATTTTCAAGAAAGATTATTAAT 331

Qy 301 TCATTTCAGAGTGGCGGCTCCGCGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCT 360
Db 332 TCATTTCAGAGTGGCGGCTCCGCGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCT 391

Qy 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 392 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 451

Qy 421 ATGCCCTGCACACGCTGCTGGGAGATCTCTGTGCCAACCCCAACGTTGGGCTTCCAGA 480
Db 452 ATGCCCTGCACACGCTGCTGGGAGATCTCTGTGCCAACCCCAACGTTGGGCTTCCAGA 511

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QY 481 GACAGCTCAGAGTTTGAGAGCATGAGGTCCATCATGATCGGAGTGGCTGAGGAAG 540
Db 512 GACAGCTCAGAGTTTGAGAGCATGAGGTCCATCATGATCGGAGTGGCTGAGGAAG 571
QY 541 AATATGGAGAGAGCCCTTTGAGAGTGCAGAGAGCAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 600
Db 572 AATATGGAGAGAGCCCTTTGAGAGTGCAGAGTGCAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 631
QY 601 GAATTCGAAGTTCTGGCCCTTTCTCAGAGAGCTGTAATGACCTGAAAGTTTCTGAAATA 660
Db 632 GAATTCGAAGTTCTGGCCCTTTCTCAGAGAGCTGTAATGACCTGAAAGTTTCTGAAATA 691
QY 661 TTGMAAACCAGAGTTAGCTGGTCTGCTGCCAAAAGAAAGCAACATGAGTTTAAAG 720
Db 692 TTGMAAACCAGAGTTAGCTGGTCTGCTGCCAAAAGAAAGCAACATGAGTTTAAAG 751
QY 721 TATCCAGTAGTATTGTAACCTGTTTTCATTTGAAAGCTGAAATATATACGTAGTCATG 780
Db 752 TATCCAGTAGTATTGTAACCTGTTTTCATTTGAAAGCTGAAATATATACGTAGTCATG 811
QY 781 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
Db 812 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 871
QY 841 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCCTTGCCGC 900
Db 872 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCCTTGCCGC 931
QY 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
Db 932 ACTGCTTGTGGTGGCTTGGCGCTC 957

RESULT 5

US-10-287-806-1

; Sequence 1, Application US/10287806

; Publication No. US20030148341A1

; GENERAL INFORMATION:

; APPLICANT: SIN, Wun Chey

; APPLICANT: YANG, Jianxin

; TITLE OF INVENTION: Gene Amplification and Overexpression in Cancer

; FILE REFERENCE: 38002-0038

; CURRENT APPLICATION NUMBER: US/10/287,806

; CURRENT FILING DATE: 2002-11-05

; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 1520

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-287-806-1

Query Match 99.7%; Score 922.8; DB 15; Length 1520;
Best Local Similarity 99.8%; Pred. No. 9.7e-277;
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCGCCGCTCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACACACAGCGCGCGGC 60
Db 366 CCCCGCCGCTCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACACACAGCGCGCGGC 425
QY 61 GCTAGCGTTCGCTTACGCCACCATGCGGAATGGATGAAACAAGATCTTCCCGCCCTGT 120
Db 426 GCTAGCGTTCGCTTACGCCACCATGCGGAATGGATGAAACAAGATCTTCCCGCCCTGT 485
QY 121 ACATCGGCAACTCNAAGATCCGAGACGCGGACATTTAGCAAGNACAGAGTGACAC 180
Db 486 ACATCGGCAACTCNAAGATCCGAGACGCGGACATTTAGCAAGNACAGAGTGACAC 545
QY 181 ATATTTCTCTGTCCACCATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
|||||

Db 546 ATATTTCTGTCTGCTCCATGATAGTCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 605
QY 241 TCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTTCAAAGAAGTATTAAAT 300
Db 606 TCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTTCAAAGAAGTATTAAAT 665
QY 301 TCATTCAGAGTGGCGCTCGCGGTGAGAGTGCCTTGTACATGCTGCTGGCCGGGTCT 360
Db 666 TCATTCAGAGTGGCGCTCGCGGTGAGAGTGCCTTGTACATGCTGCTGGCCGGGTCT 725
QY 361 CCAGAGCGTGACACTGGTGTATCATATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 726 CCAGAGCGTGACACTGGTGTATCATATCATGACCGTCACTGACTTTGGCTGGGAGG 785
QY 421 ATGCCCTGCAACCGTGTCTGGGAGATCTGTGTGCCAAACCCCAACAGCTGGGCTTCCAGA 480
Db 786 ATGCCCTGCAACCGTGTCTGGGAGATCTGTGTGCCAAACCCCAACAGCTGGGCTTCCAGA 845
QY 481 GACAGCTCCAGGAGTTTGAGAGCATGAGGTCCATCATGATCGGAGTGGCTGAGGAAG 540
Db 846 GACAGCTCCAGGAGTTTGAGAGCATGAGGTCCATCATGATCGGAGTGGCTGAGGAAG 905
QY 541 AATATGAGAGAGAGCCCTTTGAGAGTGCAGAGAGCAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 600
Db 906 AATATGAGAGAGAGCCCTTTGAGAGTGCAGAGTGCAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 965
QY 601 GAATTCGAAGTTCTGGCCCTTTCTCAGAGAGCTGTAATGACCTGAAAGTTTCTGAAATA 660
Db 966 GAATTCGAAGTTCTGGCCCTTTCTCAGAGAGCTGTAATGACCTGAAAGTTTCTGAAATA 1025
QY 661 TTGCAAAACCCAGAGTTTAGGCTGGTGGCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 720
Db 1026 TTGCAAAACCCAGAGTTTAGGCTGGTGGCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 1085
QY 721 TATCCAGTAGTATTGTAACCTGTTTTCATTTGAAAGCTGAAATATATACGTAGTCATG 780
Db 1086 TATCCAGTAGTATTGTAACCTGTTTTCATTTGAAAGCTGAAATATATACGTAGTCATG 1145
QY 781 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
Db 1146 TTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 1205
QY 841 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCCTTGCCGC 900
Db 1206 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCCTTGCCGC 1265
QY 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
Db 1266 ACTGCTTGTGGTGGCTTGGCGCTC 1291

RESULT 6

US-10-357-930-22534

; Sequence 22534, Application US/10357930

; Publication No. US20040259086A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Endege, Wilson

; APPLICANT: Monahan, John

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

; TITLE OF INVENTION: HUMAN PROSTATE CANCER

; FILE REFERENCE: MRI-007BCN

; CURRENT APPLICATION NUMBER: US/10/357,930

; CURRENT FILING DATE: 2003-02-04

; PRIOR APPLICATION NUMBER: 09/785,276

; PRIOR FILING DATE: 2003-02-16

; PRIOR APPLICATION NUMBER: 60/183,319

; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/189,862

; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/207,454

; PRIOR FILING DATE: 2000-05-25

Qy	808	TAGCAAGAGAAAATATTTTCCCTTATCCCACTCTCTGTGGAGGTTTCGTACTCGCTT	867
Db	787	TAGCAAGAGAAAATATTTTCCCTTATCCCACTCTCTGTGGAGGTTTCGTACTCGCTT	846
Qy	868	GGATGCCCTGTAAAGGATCCCGGAGCCTTGGCGCACTGCTTGTGTGGTGGCTTGGCGCTC	926
Db	847	GGATGCCCTGTAAAGATCCCGGAGCCTTGGCGCACTGCTTGTGTGGTGGCTTGGCGCTC	905
RESULT 7			
US-10-357-930-28369			
; Sequence 28369, Application US/10357930			
; Publication No. US20040259086A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Endege, Wilson			
; APPLICANT: Monahan, John			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
; TITLE OF INVENTION: HUMAN PROSTATE CANCER			
; FILE REFERENCE: MRI-007BCN			
; CURRENT APPLICATION NUMBER: US/10/357,930			
; CURRENT FILING DATE: 2003-02-04			
; PRIOR APPLICATION NUMBER: 09/785,276			
; PRIOR FILING DATE: 2003-02-16			
; PRIOR APPLICATION NUMBER: 60/183,319			
; PRIOR FILING DATE: 2000-02-17			
; PRIOR APPLICATION NUMBER: 60/189,862			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/207,454			
; PRIOR FILING DATE: 2000-05-25			
; PRIOR APPLICATION NUMBER: 60/211,314			
; PRIOR FILING DATE: 2000-06-09			
; PRIOR APPLICATION NUMBER: 60/219,007			
; PRIOR FILING DATE: 2000-07-18			
; PRIOR APPLICATION NUMBER: 60/255,281			
; PRIOR FILING DATE: 2000-12-13			
; NUMBER OF SEQ ID NOS: 62232			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 28369			
; LENGTH: 1161			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURES:			
; NAME/KEY: misc.feature			
; LOCATION: 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161			
; OTHER INFORMATION: n = A,T,C or G			
US-10-357-930-28369			
Query Match 96.6%; Score 894.2; DB 20; Length 1161;			
Best Local Similarity 99.7%; Pred. No. 7e-268;			
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0			
Qy	28	GCCATAGTGCCTTCGACACACACGGCGGGCGCTAGCGTTTCGGCTTCAGCCACCATCGG	87
Db	7	GGCCTAGTGCCTTCGACACACACGGCGGGCGCTAGCGTTTCGGCTTCAGCCACCATCGG	66
Qy	88	GGAAATGGGATGAACAAGATCTGCCCGCCCTGTATACATCGGCAACTTCAAAAGATGCCAGAG	147
Db	67	GGAAATGGGATGAACAAGATCTGCCCGCCCTGTATACATCGGCAACTTCAAAAGATGCCAGAG	126
Qy	148	ACGCGGACCAATTCGACGAAGACAAAGTGACACATATTTCTGTCTGCCACGATAGTCCA	207
Db	127	ACGCGGACCAATTCGACGAAGACAAAGTGACACATATTTCTGTCTGCCACGATAGTCCA	186
Qy	208	GGCCTATGTTGGAGGGAGTTAAATACCTGTGCATCCCAAGCAGCGGATTCACCATCTCAA	267
Db	187	GGCCTATGTTGGAGGGAGTTAAATACCTGTGCATCCCAAGCAGCGGATTCACCATCTCAA	246
Qy	268	ACCTGACAAGACATTTCAAGAAAGATATTAATTCATTCAAGATGCGGCTCCCGGGTG	327
Db	247	ACCTGACAAGACATTTCAAGAAAGATATTAATTCATTCAAGATGCGGCTCCCGGGTG	306

Qy 328 AGAGCTGCTTGTACACTGCTGCGCGGGTCTCCAGAGCGTGACACTGCTGATCCGAT 387
Db |||||
Qy 307 AGAGCTGCTTGTACACTGCTGCGCGGGTCTCCAGAGCGTGACACTGCTGATCCGAT 366
Db |||||
Qy 388 ACATCATGACCGTCACACTGCTTGGCTGGAGGATGCCCTGCACACCGTGGCTGCTGGGA 447
Db |||||
Qy 367 ACATCATGACCGTCACACTGCTTGGCTGGAGGATGCCCTGCACACCGTGGCTGCTGGGA 426
Db |||||
Qy 448 GATCCTGTGCCCAACCCCAACGCTGGCTTCCAGAGACAGCTCCAGAGTCTTGAGAGCATG 507
Db |||||
Qy 427 GATCCTGTGCCAACCCCAACGCTGGCTTCCAGAGACAGCTCCAGAGTCTTGAGAGCATG 486
Db |||||
Qy 508 AGTCCATCAGTATCGGACGTGGCTGAGAGGAATATGAGAGAGAGCCCTTTGACAGATG 567
Db |||||
Qy 487 AGTCCATCAGTATCGGACGTGGCTGAGAGGAATATGAGAGAGAGCCCTTTGACAGATG 546
Db |||||
Qy 568 CAGAAGAGCCCAAAACATCTGCGCGCTCCAGGAATCTGAACTCTGGGCTTTCTCA 627
Db |||||
Qy 547 CAGAAGAGCCCAAAACATCTGCGCGCTCCAGGAATCTGAACTCTGGGCTTTCTCA 606
Db |||||
Qy 628 GAAGACTGTATGTACCTGAAGTCTTGAATATTTGCAAAACCCGACAGTCTTAGGCTGGT 687
Db |||||
Qy 607 GAAGACTGTATGTACCTGAAGTCTTGAATATTTGCAAAACCCGACAGTCTTAGGCTGGT 666
Db |||||
Qy 688 GCTCCCAAAAGAAAGCAACATAGAGTTAAGTATCCAGTAGTATGTAAGACTTGT 747
Db |||||
Qy 667 GCTCCCAAAAGAAAGCAACATAGAGTTAAGTATCCAGTAGTATGTAAGACTTGT 726
Db |||||
Qy 748 TTTCAATTGAAGCTGAATATATAGTATAGTCAITGTTATGTTGAGAACTAAGGATATCTT 807
Db |||||
Qy 727 TTTCAATTGAAGCTGAATATATAGTATAGTCAITGTTATGTTGAGAACTAAGGATATCTT 786
Db |||||
Qy 808 TAGCAAGAGAAATATTTCCCTTATCCCACTGCTGTGAGAGTCTTGTACCTCGCTT 867
Db |||||
Qy 787 TAGCAAGAGAAATATTTCCCTTATCCCACTGCTGTGAGAGTCTTGTACCTCGCTT 846
Db |||||
Qy 868 GGATGCTGTAAGATCCGGAGGCTTGGCGCATGCTGCTTGGTGGCTTGGCGCTC 926
Db |||||
Qy 847 GGATGCTGTAAGATCCGGAGGCTTGGCGCATGCTGCTTGGTGGCTTGGCGCTC 905
Db |||||

RESULT 8

US-10-103-313-111
; Sequence 111, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PUZ07C1
; CURRENT APPLICATION NUMBER: US/10/103.313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 111
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-111

Query Match 94.6%; Score 875.8; DB 14; Length 910;
Best Local Similarity 99.8%; Pred. No. 3.4e-262;
Matches 877; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCGCGCTCCTCCTCCCTGTAAATGCCATAGTGGCCCTGGACACACACGCGCGGGC 60
Db |||||
Qy 32 CCCCGCGCTCCTCCTCCCTGTAAATGCCATAGTGGCCCTGGACACACACGCGCGGGC 91
Db |||||
Qy 61 GCTAGCGTTCGCTTACGCCACCATGGGAAATGGGATGAAACAGATCTTCCCGCGCTGT 120
Db |||||
Qy 92 GCTAGCGTTCGCTTACGCCACCATGGGAAATGGGATGAAACAGATCTTCCCGCGCTGT 151
Db |||||

Qy 121 ACATCGGCACTTCAAAGATGCCAGAGACCGGNAACAATTTAGCAAGAAACAGGTGACAC 180
Db |||||
Qy 152 ACATCGGCACTTCAAAGATGCCAGAGACCGGNAACAATTTAGCAAGAAACAGGTGACAC 211
Db |||||
Qy 181 ATATTCCTGCTGTCCACGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCA 240
Db |||||
Qy 212 ATATTCCTGCTGTCCACGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCA 271
Db |||||
Qy 241 TCCAGCAGCGGATTTCAACATCTCAAACCTGACAGACATTTCAAAGAAGTATTAAT 300
Db |||||
Qy 272 TCCAGCAGCGGATTTCAACATCTCAAACCTGACAGACATTTCAAAGAAGTATTAAT 331
Db |||||
Qy 301 TCATTACAGAGTGGCGCTCCGCGTGAGAGTGCCTTTGTACACTGCTGCGCGGGTCT 360
Db |||||
Qy 332 TCATTACAGAGTGGCGCTCCGCGTGAGAGTGCCTTTGTACACTGCTGCGCGGGTCT 391
Db |||||
Qy 361 CCAGGAGCTGACACTGCTGATCGCATCATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db |||||
Qy 392 CCAGGAGCTGACACTGCTGATCGCATCATCATGACCGTCACTGACTTTGGCTGGGAGG 451
Db |||||
Qy 421 ATGCTCTGCACACCGTGGCTGCTGGAGATCTCTGTGCCAACCCCAACGCTGGGCTTCCAGA 480
Db |||||
Qy 452 ATGCTCTGCACACCGTGGCTGCTGGAGATCTCTGTGCCAACCCCAACGCTGGGCTTCCAGA 511
Db |||||
Qy 481 GACAGCTCCAGGAGTTTGAAGCATGAGCTCCATCAGTATCGGACGTGGCTGGAAGAG 540
Db |||||
Qy 512 GACAGCTCCAGGAGTTTGAAGCATGAGCTCCATCAGTATCGGACGTGGCTGGAAGAG 571
Db |||||
Qy 541 AATATGAGAGAGAGCCCTTTGCAGGATGCAGAGAGGCGCAAAACATTTCTGGCCGCTCCAG 600
Db |||||
Qy 572 AATATGAGAGAGAGCCCTTTGCAGGATGCAGAGAGGCGCAAAACATTTCTGGCCGCTCCAG 631
Db |||||
Qy 601 GAATTCCTGAAGTCTTGGGCTTTCTCAGAAGACTGTAATGATGACCTGAAGTTTCTGAAATA 660
Db |||||
Qy 632 GAATTCCTGAAGTCTTGGGCTTTCTCAGAAGACTGTAATGATGACCTGAAGTTTCTGAAATA 691
Db |||||
Qy 661 TTGCAAAACCCGACAGTTTAGGCTGGTGGTCCCAAAAGAAAGCAACATAGAGTTTAAAG 720
Db |||||
Qy 692 TTGCAAAACCCGACAGTTTAGGCTGGTGGTGGTCCCAAAAGAAAGCAACATAGAGTTTAAAG 751
Db |||||
Qy 721 TATCCAGTGTGATTTCTGAAACTTTGTTTTCATTTGAAAGCTGAAATATATAGTGTAGTCATG 780
Db |||||
Qy 752 TATCCAGTGTGATTTCTGAAACTTTGTTTTCATTTGAAAGCTGAAATATATAGTGTAGTCATG 811
Db |||||
Qy 781 TTTATGTTGAGAACTAAGATATTTCTTTAGCAGAGAAATATTTTCCCTTATCCCGAC 840
Db |||||
Qy 812 TTTATGTTGAGAACTAAGATATTTCTTTAGCAGAGAAATATTTTCCCTTATCCCGAC 871
Db |||||
Qy 841 TGCTGTGGAGGTTTCTGTACTGCTGCTGGATGCTGTAA 879
Db |||||
Qy 872 TGCTGTGGAGGTTTCTGTACTGCTGCTGGATGCTGTAA 910
Db |||||

RESULT 9

US-10-803-738-1
; Sequence 1, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
; APPLICANT: Belmont, John
; APPLICANT: Fletcher, Frederick
; APPLICANT: Chen, Alice
; APPLICANT: Jurecic, Roland
; APPLICANT: Colicos, Suzanne
; APPLICANT: Tan, Tse-Hua
; APPLICANT: Zhou, Guisheng
; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
; FILE REFERENCE: 99-383-B
; CURRENT APPLICATION NUMBER: US/10/803.738
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/665,819A
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/155,068
; PRIOR FILING DATE: 1999-09-21

Qy 104 GATCCTGCGCGCCTGTATCATCGGCACTTCAAGATGCCAGAGACGGGGAACAATTGAG 163
 Db 513 GATCCTGCGCGCCTGTATCATCGGCACTTCAAGATGCCAGAGACGGGGAACAATTGAG 572
 Qy 164 CAAGAAACAAGGTGACACATATTTCTGTCTGTCACGATAGTCCAGGCTATGTTGGAGGG 223
 Db 573 CAAGAAACAAGGTGACACATATTTCTGTCTGTCACGATAGTCCAGGCTATGTTGGAGGG 632
 Qy 224 AGTTAAATACCTGTGCAATCCAGAGCGGATTCACCATCTCAAAACCTGACAAGACATTT 283
 Db 633 AGTTAAATACCTGTGCAATCCAGAGCGGATTCACCATCTCAAAACCTGACAAGACATTT 692
 Qy 284 CAAGAAGATTTAAATTTCAATTCAGAGTCCCGGCTCCGCGGTGAGAGCTGCCCTTGATCA 343
 Db 693 CAAGAAGATTTAAATTTCAATTCAGAGTCCCGGCTCCGCGGTGAGAGCTGCCCTTGATCA 752
 Qy 344 CTGCTGCGCGGGTCTCCAGAGCGTGACACTGCTGATGTCATCATCATCATCATCATCAT 403
 Db 753 CTGCTGCGCGGGTCTCCAGAGCGTGACACTGCTGATGTCATCATCATCATCATCATCAT 812
 Qy 404 TGACTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGCTGGGAGATCCTGTGCCAACCC 463
 Db 813 TGACTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGCTGGGAGATCCTGTGCCAACCC 872
 Qy 464 CAACGTGGGCTTCAGAGACAGCTCCAGAGTTTGAAGCATGAGTCCATCATGATGCG 523
 Db 873 CAACGTGGGCTTCAGAGACAGCTCCAGAGTTTGAAGCATGAGTCCATCATGATGCG 932
 Qy 524 GCAGTGGCTGAAGGAATATGAGAGAGCCCTTTCAGGATCGAAGAGAGCCCAAAA 583
 Db 933 GCAGTGGCTGAAGGAATATGAGAGAGCCCTTTCAGGATCGAAGAGAGCCCAAAA 992
 Qy 584 CATCTCG 591
 Db 993 CATCTCG 1000

RESULT 12
 US-10-803-738-3
 ; Sequence 3, Application US/10803738
 ; Publication No. US2005001422A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Belmont, John
 ; APPLICANT: Fletcher, Frederick
 ; APPLICANT: Chen, Alice
 ; APPLICANT: Jurecic, Roland
 ; APPLICANT: Colicos, Suzanne
 ; APPLICANT: Tan, Tee-Hua
 ; APPLICANT: Zhou, Guisheng
 ; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
 ; FILE REFERENCE: 99-383-B
 ; CURRENT APPLICATION NUMBER: US/10/803,738
 ; CURRENT FILING DATE: 2004-03-18
 ; PRIOR APPLICATION NUMBER: US/09/665,819A
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US 60/155,068
 ; PRIOR FILING DATE: 1999-09-21
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 3010
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (15)..(629)
 ; OTHER INFORMATION: n is a, t, c, or g
 Query Match 45.2%; Score 418.6; DB 21; Length 3010;
 Best Local Similarity 87.7%; Pred. No. 4e-119;
 Matches 457; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 US-10-803-738-3

Qy 71 GCCTTCAGCCACCATTGGGGAATGGGATGAACAAGATCCTGCCCGGCTGTACATCGCAA 130
 Db 2 GCCCGGCGCGCCATTGGGAGATGGAGATGAGCCAGATCCTGCCCGGCTGTACATCGCAA 61
 Qy 131 CTTCAAAAGATGCGCAGAGACGCGAAACAATTTGAGCAAGAAACAAGGTGACACATATTTCTGTC 190
 Db 62 CTTCAAAAGATGCGCAGAGATGCGAAACAAGTTGAGCAGGAAACAAGGTGACACATATTTCTTTC 121
 Qy 191 TGTCCACGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCAATCCAGCAGC 250
 Db 122 TGTGACGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGATATTCAGCGGC 181
 Qy 251 GGATTACCATCTCAAAACCTGACAAGACATTTCAAGAAAGTATTTAAATTCATTACGA 310
 Db 182 AGACACACCATCTCAAAACCTGACAAGACATTTCAAGAAAGTATTTAAATTCATTACGA 241
 Qy 311 GTGCCGCTCCGGGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCTCCAGAGAGGT 370
 Db 242 GTGCCGCTCCGGGTGAGAGCTGCTTTGTACACTGCTGCGCGGGTCTCCAGAGAGGT 301
 Qy 371 GACACTGGTATCGCATATCATGACCGTCACTGACTTTGGCTGGAGGATGCCCTGCA 430
 Db 302 GACATTGGTATCGCATATCATGACCGTCACTGACTTTGGCTGGAGAGATGCCCTGCA 361
 Qy 431 CACGCTGCTGCTGGAGATCCTGTGCCAACCCCAACGTTGGGCTCCAGAGACAGCTCCA 490
 Db 362 CACTGTTGCTGCGGGAGGTCTGTGCCAACCCCAACGTTGGGCTTTCAAAGGCGAGCCGA 421
 Qy 491 GGAGTTTGAAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGTATGGAGA 550
 Db 422 GGAGTTTGAAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGTATGGAGA 481
 Qy 551 GAGCCCTTTGCAGGATCGAAGAGCCAAACCAATTCCTGG 591
 Db 482 GAACCTTTGCGGATCGAAGAGCCAAACCAATTCCTGG 522

RESULT 13
 US-10-101-510-481
 ; Sequence 481, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; APPLICANT: WANG, YIXIN
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/10/101,510
 ; CURRENT FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: 60/276,947
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 481
 ; LENGTH: 2420
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified base
 ; LOCATION: (906)..(1002)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-101-510-481
 Query Match 40.5%; Score 375.4; DB 15; Length 2420;
 Best Local Similarity 89.5%; Pred. No. 1.1e-105;
 Matches 436; Conservative 0; Mismatches 1; Indels 50; Gaps 1;
 Qy 105 ATCCTGCGCGCCTGTATCATCGGCAACTTCAAGATGCCAGAGACGGGACAAATTGAGC 164
 Db 1 ATCCTGCGCGCCTGTATCATCGGCAACTTCAAGATGCCAGAGACGGGACAAATTGAGC 60
 Qy 165 AAGAAACAAGGTGACACATATTTCTGTGTCACCATAGTCCAGGCTATGTTGGAGGGA 224
 Db 61 AAGAAACAAGGTGACACATATTTCTGTGTCACCATAGTCCAGGCTATGTTGGAGGGA 117

QY	225	GTAAATACCTGTGCATCCACGACGGGATTCACCATCTCAAAACCTGACAAAGCATTTTC	284
Db	118	-----GACAAAGCATTTTC	130
QY	285	AAAGAAAGTATTAAATTCATTCCACGAGTCCCGGCTCCCGGCTGAGAGCTGCCTTGTACAC	344
Db	131	AAAGAAAGTATTAAATTCATTCCACGAGTCCCGGCTCCCGGCTGAGAGCTGCCTTGTACAC	190
QY	345	TGCTGGCCGGGCTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACT	404
Db	191	TGCTGGCCGGGCTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACT	250
QY	405	GACTTTGGCTGGAGGATGSCCTCGCACACCGTGGCTGGGAGATCCTGTGCCAACCC	464
Db	251	GACTTTGGCTGGAGGATGSCCTCGCACACCGTGGCTGGGAGATCCTGTGCCAACCC	310
QY	465	AACGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGG	524
Db	311	AACGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGG	370
QY	525	CAGTGGCTGAAGGAAGAATATGAGAGAGCCCTTTTCAGGATGCAGAAGAACCCAAAAAC	584
Db	371	CAGTGGCTGAAGGAAGAATATGAGAGAGCCCTTTTCAGGATGCAGAAGAACCCAAAAAC	430
QY	585	ATTCTGG	591
Db	431	ATTCTGG	437

Qy	831	TTATCCCGCACTGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCCCTGTAAAGGATCCCGGA	890
Db	287	TTATCCCGCACTGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCCCTGTAAAGGATCCCGGA	346
Qy	891	GCCTTGCGCACTGCTGTGGGTTGGCTTGGCGCTC	926
Db	347	GCCTTGCGCACTGCTGTGGGTTGGCTTGGCGCTC	382

Search completed: July 21, 2005, 18:51:59
Job time : 727 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 07:55:30 ; Search time 3729 Seconds
(without alignments)
9452.270 Million cell updates/sec

Title: US-10-658-661-1

Perfect score: 926

Sequence: 1 cccgcgcgtctctctccct.....ttgtgggtggcttgccgc 926

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	869.8	93.9	1066	3	CR596349 full-leng
2	853	92.1	1060	5	BX358385
3	796	86.0	895	5	BQ225790 AGENCOURT
4	763.8	82.5	879	5	BQ181268 AGENCOURT
5	755.8	81.6	953	5	BX358384
6	712.2	76.9	717	1	AV714942 AV714942
7	705	76.1	758	4	BI908832 603066403
8	681	73.5	915	2	BE868556 601444589
9	653.8	70.6	665	4	BG532390 602561902
10	644.2	69.6	694	1	AV764304 AV764304
11	622.4	67.2	655	6	CD693732 EST10255
12	607	65.6	819	6	CB995799 AGENCOURT
13	582.4	62.9	930	6	CA453928 AGENCOURT
14	569.4	61.5	751	4	BG545679 602572945
15	566	61.1	712	7	CR394735 170006001
16	560	60.5	845	5	BUI98761 DCBCQF01
17	554.4	59.9	835	5	BU603622 AGENCOURT
18	548.4	59.2	1038	5	BM922798 AGENCOURT
19	541	58.4	1088	5	BM920978 AGENCOURT
20	540.4	58.4	819	2	BE910217 601503530
21	536.4	57.9	538	6	CB215017 NISC np01
22	536.4	57.9	950	4	BG674814 602620947
23	502.2	54.2	784	7	CR792116 DKFZp469M
24	496.4	53.6	1087	5	BQ894734 AGENCOURT

C 25	494.8	53.4	715	5	BM982838	BM982838	UI-CF-EN1
C 26	493.2	53.3	715	5	BQ018732	BQ018732	UI-H-DH1-
C 27	491.2	53.0	716	6	CB852535	CB852535	UI-CF-FN0
C 28	489	52.8	504	6	CD629904	CD629904	56051849H
C 29	487.4	52.6	505	6	CD629905	CD629905	56051849H
30	479	51.7	600	4	BG800196	BG800196	2113-90 M
31	469.4	50.7	713	4	BM018391	BM018391	603646072
32	462.8	50.0	715	7	CN842339	CN842339	AGENCOURT
33	453.2	48.9	589	2	AW963729	AW963729	EST375902
34	451.4	48.7	574	5	BQ416267	BQ416267	i53a04.Y
35	450	48.6	1108	4	BM541277	BM541277	AGENCOURT
36	443.8	47.9	447	1	AA410486	AA410486	v233D12.r
37	433.8	46.8	859	4	BI829670	BI829670	603079718
38	421.8	45.6	2252	3	BC080718	BC080718	Mus muscu
39	421.4	45.5	569	4	BI158161	BI158161	602920611
40	411.4	44.4	522	6	CB720826	CB720826	AMGNNUC:N
41	410.2	44.3	528	5	BQ416291	BQ416291	i153c10.Y
42	394.8	42.6	651	5	BUI82790	BUI82790	AGENCOURT
43	394.6	42.6	510	6	CA034663	CA034663	4000292 B
44	392.2	42.4	734	4	BG697122	BG697122	602660343
45	390.4	42.2	477	6	CA407076	CA407076	1003225 H

ALIGNMENTS

RESULT 1	CR596349	1066 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSODI037YC10 of Placent	Cot 25-normalized			
DEFINITION	of Homo sapiens (human)				
ACCESSION	CR596349				
VERSION	CR596349.1 GI:50477156				
KEYWORDS	HTC; CNSLT_cDNA				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1066)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..1066				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CSODI037YC10"				
	/tissue_type="Placenta				
	/plasmid="pCMVSPORT_6"				

Query Match 93.9%; Score 869.8; DB 3; Length 1066;
Best Local Similarity 99.8%; Pred. No. 2.8e-243;
Matches 871; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

54	CCGGGGCGCTAGCGTTCGCTTACGCCACCCATGGGGAATGGATGAACAAGATCTGCCC	113
1	CCGGGGCGCTAGCGTTCGCTTACGCCACCCATGGGGAATGGATGAACAAGATCTGCCC	60

QY	114	GGCCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAAACAATTGAGCAAGAACAG	173
Db	61	GGCCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAAACAATTGAGCAAGAACAG	120
QY	174	GTGACACATATCTCTGTCTCCACATAGTCACGCGCTATGTTGGAGGGAGTTAAATAC	233
Db	121	GTGACACATATCTCTGTCTCCACATAGTCACGCGCTATGTTGGAGGGAGTTAAATAC	180
QY	234	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGT	293
Db	181	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGT	240
QY	294	ATTAAATTCATTCAGAGTCGGCTCCGCGTGAGAGCTGCTTGTACACTGCTGGCC	353
Db	241	ATTAAATTCATTCAGAGTCGGCTCCGCGTGAGAGCTGCTTGTACACTGCTGGCC	300
QY	354	GGGGTCTCCAGAGCGTGACACTGTGTGATCGCATATCATGACCGTCACCTGCTTGGC	413
Db	301	GGGGTCTCCAGAGCGTGACACTGTGTGATCGCATATCATGACCGTCACCTGCTTGGC	360
QY	414	TGGAGGATGCCCTGCACACCGTGCTGTGGAGATCCTGTGCCAACCCCAACGTGGCC	473
Db	361	TGGAGGATGCCCTGCACACCGTGCTGTGGAGATCCTGTGCCAACCCCAACGTGGCC	420
QY	474	TTCAGACACACTCCAGAGTTTGAAGAGCATGAGTCCATCAGTATCGGCAGTGGCTG	533
Db	421	TTCAGACACACTCCAGAGTTTGAAGAGCATGAGTCCATCAGTATCGGCAGTGGCTG	480
QY	534	AAGGAAGATATGGAGAGCGCTTTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAG	593
Db	481	AAGGAAGATATGGAGAGCGCTTTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAG	540
QY	594	GCTCAGGAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGTACCTGAAGTTTC	653
Db	541	GCTCAGGAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGTACCTGAAGTTTC	600
QY	654	TGAATATATGMAACCCGAGAGTTTAGCTGGTCTGCCAAAAGGAGGAGGAGGAGGAG	713
Db	601	TGAATATATGMAACCCGAGAGTTTAGCTGGTCTGCCAAAAGGAGGAGGAGGAGGAG	660
QY	714	GTTTAAGTATCAGTAGTATTTGTAAGCTTTTTCATTTGAGCTGAATATATACGT	773
Db	661	GTTTAAGTATCAGTAGTATTTGTAAGCTTTTTCATTTGAGCTGAATATATACGT	720
QY	774	AGTCAATTTATGTTGAGAACTAAGGATTAATCTTTAGCAAGAGAAATATTTTCCCTTA	833
Db	721	AGTCAATTTATGTTGAGAACTAAGGATTAATCTTTAGCAAGAGAAATATTTTCCCTTA	780
QY	834	TCCCACTGCTGTGGAGGTTTCTGTACCTCGCTGGATGCTGTAAGGATCCCGGAGCC	893
Db	781	TCCCACTGCTGTGGAGGTTTCTGTACCTCGCTGGATGCTGTAAGGATCCCGGAGCC	840
QY	894	TGCGGCACTGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	926
Db	841	TGCGGCACTGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	873
RESULT 2			
LOCUS	BX358385	1060 bp	mRNA linear EST 08-APR-2004
DEFINITION	BX358385 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	clone CS01037YC10 5-PRIME, mRNA sequence.		
VERSION	BX358385.2	GI:46304699	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
	Full-length cDNA libraries and normalization		

JOURNAL COMMENT

Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376226.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3530.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS01037B05QPl&c=3530.f.

FEATURES source

Location/Qualifiers
1..1060
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS01037YC10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match	92.1%;	Score 853;	DB 5;	Length 1060;
Best Local Similarity	99.3%;	Pred. No. 2.4e-238;		
Matches 867;	Conservative 0;	Mismatches 5;	Indels 1;	Gaps 1;
QY	54	CCGGGGCGCTAGGCTTCGCTTCAGCACCATGGGGAATGGGATGAACAAGATCCTGCC	113	
Db	2	CGGGATCGCTAGGCTTCGCTTCAGCACCATGGGGAATGGGATGAACAAGATCCTGCC	61	
QY	114	GGCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAAACAATTGAGCAAGAACAG	173	
Db	62	GGCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAAACAATTGAGCAAGAACAG	121	
QY	174	GTGACACATATCTCTGTCTCCAGATAGTCCAGGCTATGTTGGAGGGAGTTAAATAC	233	
Db	122	GTGACACATATCTCTGTCTCCAGATAGTCCAGGCTATGTTGGAGGGAGTTAAATAC	181	
QY	234	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGT	293	
Db	182	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGT	241	
QY	294	ATTAAATTCATTCAGAGTCGGCTCCGCGTGAGAGCTGCTTGTACACTGCTGGCC	353	
Db	242	ATTAAATTCATTCAGAGTCGGCTCCGCGTGAGAGCTGCTTGTACACTGCTGGCC	301	
QY	354	GGGCTCTCCAGGAGCGTGACACTGGTGATCGCATATCATGACCGTCACCTGCTTGGC	413	
Db	302	GGGCTCTCCAGGAGCGTGACACTGGTGATCGCATATCATGACCGTCACCTGCTTGGC	361	
QY	414	TGGAGAGATGCTGACACCGTGGCTGTGGAGATGCTGTGCCAACCCCAACGTGGCC	473	
Db	362	TGGAGAGATGCTGACACCGTGGCTGTGGAGATGCTGTGCCAACCCCAACGTGGCC	421	
QY	474	TTCAGAGAGAGCTCCAGGAGTTTGAGAAGCATGAGTCCATCATGATCCGAGTGGCTG	533	
Db	422	TTCAGAGAGAGCTCCAGGAGTTTGAGAAGCATGAGTCCATCATGATCCGAGTGGCTG	481	
QY	534	AAGGAAGATATGGAGAGCGCTTTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAG	593	
Db	482	AAGGAAGATATGGAGAGCGCTTTTGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAG	541	
QY	594	GCTCAGGAATTTGAAAGTTCTGGGCTTTCTCAGAAAGACTGTAATGTACTGAAGTTTC	653	
Db	542	GCTCAGGAATTTGAAAGTTCTGGGCTTTCTCAGAAAGACTGTAATGTACTGAAGTTTC	601	
QY	654	TGAATATATGCMAACCCGAGAGTTTAGCTGGTCTGCCAAAAGGAGGAGGAGGAGGAG	712	

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Db      602 TGAATATTGCAACCCACAGAGTTAGCTGGTGCCTGCAAAAGAAAGCAACATAAG 661
      |||
Qy      713 AGTTTAAGTATCCAGTAGTGAATTTGTAAGTGTGTTTTCATTGAGCTGATATATAGG 772
      |||
Db      662 AGTTTAAGTATCCAGTAGTGAATTTGTAAGTGTGTTTTCATTGAGCTGATATATAGG 721
      |||
Qy      773 TAGTCATGTTTATGTTGAGAACTAAGGATATTTCTTAGCAAGAGAAATATTTTCCCTTT 832
      |||
Db      722 TAGTCATGTTTATGTTGAGAACTAAGGATATTTCTTAGCAAGAGAAATATTTTCCCTTT 781
      |||
Qy      833 ATCCCACTGCTGTGGAGTTTCTGTACCTGCTTGGATGCTGTGAAGATCCCGGAGC 892
      |||
Db      782 ATCCCACTGCTGTGGAGTTTCTGTACCTGCTTGGATGCTGTGAAGATCCCGGAGC 841
      |||
Qy      893 CTTGCCGCACTGCTTGTGGGTTGGCTTGGCGCT 925
      |||
Db      842 CTTGCCGCACTGCTTGTGGGTTGGCTTGGCGCT 874
      |||

RESULT 3
B0225790
LOCUS      B0225790
DEFINITION AGENCOURT_758986 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070216
5', mRNA sequence.
ACCESSION B0225790
VERSION   B0225790.1 GI:20407190
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 895)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NIH-MGC http://mgi.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DP/Gapdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLM13354 row: c column: 17
          High quality sequence stop: 589.
          Location/Qualifiers
            1. .895
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6070216"
              /tissue_type="large cell carcinoma"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC 68"
              /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
              Average insert size 1.8 Kb. Library constructed by Life
              Technologies."
          ORIGIN
            Query Match      86.0%; Score 796; DB 5; Length 895;
            Best Local Similarity 98.7%; Pred. No. 1.2e-221;
            Matches 813; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy      101 CAAGATCTCTGCCGGCTGTACATCGGCACTTCAAGATGCGCAGAGCGCGAACAATT 160
      |||
Db      1   CAAGATCTCTGCCGGCTGTACATCGGCACTTCAAGATGCGCAGAGCGCGAACAATT 60
      |||
Qy      161 GAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATAGTCGAGCGCTATGTGGA 220
      |||
Db      61  GAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATAGTCGAGCGCTATGTGGA 120
      |||

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Qy      221 GGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTACCATCTCTCAAAACCTGACAAGACA 280
      |||
Db      121 GGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTACCATCTCTCAAAACCTGACAAGACA 180
      |||
Qy      281 TTTCAAGAAAAGTATTAAATTCATTCACAGTGC CGGCTCCGCGGTGAGAGCTGCTTGT 340
      |||
Db      181 TTTCAAGAAAAGTATTAAATTCATTCACAGTGC CGGCTCCGCGGTGAGAGCTGCTTGT 240
      |||
Qy      341 ACATCTGCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATACATCATGACCGT 400
      |||
Db      241 ACATCTGCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATACATCATGACCGT 300
      |||
Qy      401 CACTGACTTTTGGCTGGGAGGATGCCCTGTCACACCGTGCCTGCTGGGAGATCTCTGTGCCAA 460
      |||
Db      301 CACTGACTTTTGGCTGGGAGGATGCCCTGTCACACCGTGCCTGCTGGGAGATCTCTGTGCCAA 360
      |||
Qy      461 CCCCAACGTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATGAGGTCATCAGTA 520
      |||
Db      361 CCCCAACGTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATGAGGTCATCAGTA 420
      |||
Qy      521 TCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCGAGGATGAGAGAGCCCAA 580
      |||
Db      421 TCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCGAGGATGAGAGAGCCCAA 480
      |||
Qy      581 AAACATTTCTGGCCGCTCCAGGAATTTCTGAAGTTCTTGGGCCCTTTCTCAGAAGACTGTAATG 640
      |||
Db      481 AAACATTTCTGGCCGCTCCAGGAATTTCTGAAGTTCTTGGGCCCTTTCTCAGAAGACTGTAATG 540
      |||
Qy      641 TACCTGAAGTTTCTGAATATTTGCAAAACCCGACAGTTTAGGCTGGTCTGCCAAAAAGA 700
      |||
Db      541 TACCTGAAGTTTCTGAATATTTGCAAAACCCGACAGTTTAGGCTGGTCTGCCAAAAAGA 600
      |||
Qy      701 AAAGCAACATAGATTTTAAGTATCCAGTAGTGAATTTGTAAGTTGTTTAACTTGTTCATTGGAAGC 760
      |||
Db      601 AAAGCAACATAGATTTTAAGTATCCAGTAGTGAATTTGTAAGTTGTTTAACTTGTTCATTGGAAGC 660
      |||
Qy      761 TGAATATATACCTAGTCAATGTTTATGTTGAGAACTTAAGGATATTTCTTAGCAAGAGAAAA 820
      |||
Db      661 TGAATATATACCTAGTCAATGTTTATGTTGAGAACTTAAGGATATTTCTTAGCAAGAGAAAA 720
      |||
Qy      821 TATTTTCCCTTATCCCACTGCTGTGGAGTTTCTGTACCTCGCTGGATGCTGCTGTGAAG 880
      |||
Db      721 TATTTTCCCTTATCCCACTGCTGTGGAGTTTCTGTACCTCGCTGGATGCTGCTGTGAAG 780
      |||
Qy      881 GATCCC-GGAGAGCTTGGCGCACTGCCTTGTGGGTGGCTTGGCG 923
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Db      781 GATCCCGGGGACCTTGGCGCACTGCCTTGGGGGGGGGCTTGGG 824
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RESULT 4
BUI1268
LOCUS      BUI1268
DEFINITION AGENCOURT_7938918 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6008665
5', mRNA sequence.
ACCESSION BUI1268
VERSION   BUI1268.1 GI:22695252
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 879)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NIH-MGC http://mgi.nci.nih.gov/.
COMMENT   National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DP/Gapdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be

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QY 377 GGTGATCGCATACATCATGACCGTCACTGACATTTGGCTGGGAGGATGCCCTGCACACCGT 436
Db 714 GGTGATCGCATACATCATGACCGTCACTGACATTTGGCTGGGAGGATGCCCTGCACACCGT 655
QY 437 GGTGCTGGGAGATCTGTGCCAACCCCAACCTGGCTGGGCTTCAGAGACAGCTCCAGGATTT 496
Db 654 GGTGCTGGGAGATCTGTGCCAACCCCAACCTGGCTGGGCTTCAGAGACAGCTCCAGGATTT 595
QY 497 TCAGAGCATGAGTTCATGATCGGAGTTCGAGGAGTTCGAGGAGGAGTTCGAGGAGGAGTTC 556
Db 594 TCAGAGCATGAGTTCATGATCGGAGTTCGAGGAGTTCGAGGAGGAGTTCGAGGAGGAGTTC 535
QY 557 TTTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 616
Db 534 TTTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475
QY 617 GGCCTTTCTCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
Db 474 GGCCTTTCTCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
QY 677 TTTAGGCTGGTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
Db 414 TTTAGGCTGGTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355
QY 736 TGTAACTTTGTTTTCATTTGAAGCTGATATATATATATATATATATATATATATATATATAT 795
Db 354 TGTAACTTTGTTTTCATTTGAAGCTGATATATATATATATATATATATATATATATATATAT 295
QY 796 AAGGATATCTTTAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 855
Db 294 AAGGATATCTTTAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235
QY 856 TGTACTCGCTGGATGCTGTAAGGATCCCGGAGGCTTGCAGCAGCTGCTGCTGGGCTG 915
Db 234 TGTACTCGCTGGATGCTGTAAGGATCCCGGAGGCTTGCAGCAGCTGCTGCTGGGCTG 175
QY 916 GCTTGGCGCT 925
Db 174 GCTTGGCGCT 165

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RESULT 6
AV714942
LOCUS AV714942 DCB Homo sapiens cDNA clone DCBBJE09 5', mRNA sequence.
DEFINITION AV714942
ACCESSION AV714942.1 GI:10796459
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Xu,X., Gu,J., Liu,P., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Cheng,Z. and Han,Z.
TITLE Homo sapiens cDNA DCB clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguogang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

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FEATURES
source
location/Qualifiers
1..717
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="DCBBJE09"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplEx2; Site_1: sfIIA; Site_2: sfIIB"

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ORIGIN
Query Match 76.9%; Score 712.2; DB 1; Length 717;
Best Local Similarity 99.6%; Pred. No. 4.1e-197;
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 100 ACAAGATCTCCCGGCTGTACATCGGCAATCTCAAGATGCGAGAGACCGGAAACAAT 159
Db 1 ACAAGATCTCCCGGCTGTACATCGGCAATCTCAAGATGCGAGAGACCGGAAACAAT 60
QY 160 TGAGCAAGAACAGGTGACACATATCTGTCTGTCACAGTAGTGCCAGGCTATGTTGG 219
Db 61 TGAGCAAGAACAGGTGACACATATCTGTCTGTCACAGTAGTGCCAGGCTATGTTGG 120
QY 220 AGGAGTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGAC 279
Db 121 AGGAGTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGAC 180
QY 280 ATTTCAAGAAAGTAAATTAATTCATTCAGAGTCCCGGCTCCGCGGTGAGAGTGCCTTG 339
Db 181 ATTTCAAGAAAGTAAATTAATTCATTCAGAGTCCCGGCTCCGCGGTGAGAGTGCCTTG 240
QY 340 TACACTGCTGGCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCG 399
Db 241 TACACTGCTGGCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCG 300
QY 400 TCAGTACTTTGGCTGGGAGGATCCCTGCACACCGTGCCTGGGAGATCCCTGTGCGCA 459
Db 301 TCAGTACTTTGGCTGGGAGGATCCCTGCACACCGTGCCTGGGAGATCCCTGTGCGCA 360
QY 460 ACCCAACGTGGGCTTCAGAGACAGCTCCAGAGGATTTGAGAAGCATGAGGTCCATCAGT 519
Db 361 ACCCAACGTGGGCTTCAGAGACAGCTCCAGAGGATTTGAGAAGCATGAGGTCCATCAGT 420
QY 520 ATCGGCGAGTGGCTGAAGAGAGATATGAGAGAGCGCTTTTCAGAGATGCGAGAGGCGCA 579
Db 421 ATCGGCGAGTGGCTGAAGAGAGATATGAGAGAGCGCTTTTCAGAGATGCGAGAGGCGCA 480
QY 580 AAAACATCTGCGCGCTCCAGGAAATCTGAAGTTCTGGGCTTCTCAGAGAGCTGTAAT 639
Db 481 AAAACATCTGCGCGCTCCAGGAAATCTGAAGTTCTGGGCTTCTCAGAGAGCTGTAAT 540
QY 640 GTACTGAAAGTTTCTGAAATATTTGCAACCCGAGAGTTTAGGCTGGTGGTCCCAAAAG 699
Db 541 GTACTGAAAGTTTCTGAAATATTTGCAACCCGAGAGTTTAGGCTGGTGGTCCCAAAAG 600
QY 700 AAAAGCAACATAGAGTTTAAGTATCCAGTAGTATGTTGTAACCTGTTTTCATTTGAAG 759
Db 601 AAAAGCAACATAGAGTTTAAGTATCCAGTAGTATGTTGTAACCTGTTTTCATTTGAAG 660
QY 760 CTGAATATATACGTAAGTATGTTGTAAGTATGTTGTAAGTATGTTGTAAGTATGTTGTAAG 816
Db 661 CTGAATATATACGTAAGTATGTTGTAAGTATGTTGTAAGTATGTTGTAAGTATGTTGTAAG 717

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RESULT 7
BI908832
LOCUS BI908832
DEFINITION 603066403F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215465 5',
mRNA sequence.
ACCESSION BI908832
VERSION BI908832.1 GI:16171910
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 758)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11541 row: e column: 02
High quality sequence stop: 736.
Location/Qualifiers
1..758
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5215465"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

FEATURES
source
1..758
Location/Qualifiers
1..758
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5215465"
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/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 76.1%; Score 705; DB 4; Length 758;
Best Local Similarity 98.5%; Pred. No. 5.4e-195;
Matches 722; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 195 CACGATAGTGCAGCGCTATGTGGAGGAGTTAAATACCTGTGTCATCCCGAGCGGAT 254
Db 1 CACGATAGTGCAGCGCTATGTGGAGGAGTTAAATACCTGTGTCATCCCGAGCGGAT 60
QY 255 TCACCATCTCAAACTGACAGACATTTCAAAGAAAGTATTAATTCATTACAGATGC 314
Db 61 TCACCATCTCAAACTGACAGACATTTCAAAGAAAGTATTAATTCATTACAGATGC 120
QY 315 CGGCTCCGGGTGAGAGTGCCTTGTACACTGCTGGCGGGGTCTCCAGGAGCGTGACA 374
Db 121 CGGCTCCGGGTGAGAGTGCCTTGTACACTGCTGGCGGGGTCTCCAGGAGCGTGACA 180
QY 375 CTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGAGGATGCCCTGCACACC 434
Db 181 CTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGAGGATGCCCTGCACACC 240
QY 435 GTGCTGTCTGGAGATCTGTGTCACACCCACGCTGGGCTTCCAGAGACAGCTCCAGAG 494
Db 241 GTGCTGTCTGGAGATCTGTGTCACACCCACGCTGGGCTTCCAGAGACAGCTCCAGAG 300
QY 495 TTTGAGAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGATATGGAGAGGC 554
Db 301 TTTGAGAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGATATGGAGAGGC 360
QY 555 CTTTTCAGGATGCAGAGAGAGCCAAAAACATTTCTGGCCGCTTCCAGGAAATTTCTGAAGTTC 614
Db 361 CTTTTCAGGATGCAGAGAGAGCCAAAAACATTTCTGGCCGCTTCCAGGAAATTTCTGAAGTTC 420
QY 615 TGGGCTTTCTCAGAAAGACTGTATGTACCTGAAGTTTCTGAA-ATATTGCAAAACCCGCA 673
Db 421 TGGGCTTTCTCAGAAAGACTGTATGTACCTGAAGTTTCTGAAACATATTGCAAAACCCGCA 480
QY 674 GAGTTTAGTCTGCTGCAAAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGA 733
Db 733

Db 481 GAGTTTAGTCTGCTGCCAAAAAGAAAGCAACATAGAGTTTAACTATCCAGTAGTGA 540
QY 734 TTTGTAACCTGTTTTCATTTGAAGCTGAATATATACGTAGTCATGTTTATGTTAGAA 793
Db 541 TTTGTAACCTGTTTTCATTTGAAGCTGAATATATACGTAGTCATGTTTATGTTAGAA 600
QY 794 CTAAGGATATTTCTTAGCAAGAGAAAATATTTTCCCTTATCCCACTGCTGTGGAGGTT 853
Db 601 CTAAGGATATTTCTTAGCAAGAGAAAATATTTTCCCTTATCCCACTGCTGTGGAGGTT 660
QY 854 TCTGTACTCGCTTGGATGCTGTGAAGATCCCGGAGCCTTGGCGACCTGCTTGTGGG 913
Db 661 ACTGTACTCGCTTGGATGCTGTGAAGATCCCGGAGCCTTGGCGACCTGCTTGTGGG 720
QY 914 TGGCTTGGCGCTC 926
Db 721 TGGCTTGGCGCTC 733

RESULT 8
BE868556
LOCUS 601444589F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848374 5',
DEFINITION mRNA sequence.
ACCESSION BE868556
VERSION BE868556.1 GI:10317332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9564 row: b column: 23
High quality sequence stop: 693.
Location/Qualifiers
1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3848374"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_65"
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN
Query Match 73.5%; Score 681; DB 2; Length 915;
Best Local Similarity 92.6%; Pred. No. 6.2e-188;
Matches 749; Conservative 0; Mismatches 55; Indels 5; Gaps 3;
QY 86 GGGGAATGGGATGAACAAAGATCTTCCCGCTGTACATCGCAACTTCAAGATGCGAG 145
Db 8 GGGGAATGGGATGAACAAAGATCTTCCCGCTGTACATCGCAACTTCAAGATGCGAG 67
QY 146 AGACGCGGAACAATTTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATGTC 205
Db 68 AGACGCGGAACAATTTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATGTC 127

206 CAGGCGCTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 265
Db |||||
128 CAGGCGCTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 187
Qy |||||
266 AAACCTGACAGACATTTCAAGAAAGTATTAAATTCATTACGAGTCCGGCTCCGGCG 325
Db |||||
188 AAACCTGACAGACATTTCAAGAAAGTATTAAATTCATTACGAGTCCGGCTCCGGCG 247
Qy |||||
326 TGAGAGCTGCTTGTACACTGCTCGCGGGGTCTCCAGGAGCGTGACACTGGTGATCGC 385
Db |||||
248 TGAGAGCTGCTTGTACACTGCTCGCGGGGTCTCCAGGAGCGTGACACTGGTGATCGC 307
Qy |||||
386 ATACATCATGACCGCTCACTGACTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGG 445
Db |||||
308 ATACATCATGACCGCTCACTGACTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGG 367
Qy |||||
446 GAGATCCTGTGCCAACCCACCGTGGCTTCAGAGACAGCTCCAGGAGTTTGAGAGCA 505
Db |||||
368 GAGATCCTGTGCCAACCCACCGTGGCTTCAGAGACAGCTCCAGGAGTTTGAGAGCA 427
Qy |||||
506 TGAGGTCCATCAGTATCGCAGTGGCTGAAGGAAGATATGAGAGAGCCCTTTGCAGGA 565
Db |||||
428 TGAGGTCCATCAGTATCGCAGTGGCTGAAGGAAGATATGAGAGAGCCCTTTGCAGGA 487
Qy |||||
566 TCCAGAGAGCCAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCT 625
Db |||||
488 TCCAGAGAGCCAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCT 547
Qy |||||
626 CAGAGACTGTAATGTAAGTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTT 685
Db |||||
548 CAGAGACTGTAATGTAAGTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTT 607
Qy |||||
686 GTGCTGCCAAAGAAAGAACACATAGAGTTTAAGTATCCAGTATGATTTGTAACCTG 745
Db |||||
608 GTGCTGCCAAAGAAAGAACACATAGAGTTTAAGTATCCAGTATGATTTGTAACCTG 666
Qy |||||
746 TTTTTCATTTGAAGCTGAATATATACGTAGTATCATGTTTATGTTGAGAACTAAGGATATTC 805
Db |||||
667 GATTTTCATTTGAGCTG-ATATATAGTAGTATGATGTCAGCTCGAGAACTCAGGATATTC 725
Qy |||||
806 TTTAGCAAGAGAAATATTTTCCCTTATCCCACTGCTGTGGAGGTTTCTGTACCTCGC 865
Db |||||
726 TTAAGC---AGAGAAACATTTCCCTTAATCCCACTGCTGTGGAGGTTTCTGTACCTCGC 782
Qy |||||
866 TTGGATGCTGTGAAGATCCCGGAGCT 894
Db |||||
783 TTGAGAGCTGTGAAGATCCCGGAGCTT 811

RESULT 9
BG532390 665 bp mRNA linear EST 03-APR-2001
LOCUS 602561902F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699705 5',
DEFINITION mRNA sequence.
ACCESSION BG532390
VERSION BG532390.1 GI:13523928
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 665)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCMI532 row: c column: 02
High quality sequence stop: 663.
FEATURES
Location/Qualifiers
source
1..665
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4699705"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTATGAGCGCGGCGGCATG-dt(30)BN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match. 70.6%; Score 653.8; DB 4; Length 665;
Best Local Similarity 98.9%; Pred. No. 5.3e-180;
Matches 658; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 56 GGGCGCTAGCGCTTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCCCGG 115
Db 1 GGGCGCTAGCGCTTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCCCGG 60
Qy 116 CCTGTACATCGGCAACTTCAAGATGCCAGAGACGGGAAACAATTGAGCAAGAGT 175
Db 61 CCTGTACATCGGCAACTTCAAGATGCCAGAGACGGGAAACAATTGAGCAAGAGT 120
Qy 176 GACACATATCTGTCTGCCAGATAGTCCAGGCTATGTTGGAGGAGTTAATACCT 235
Db 121 GACACATATCTGTCTGCCAGATAGTCCAGGCTATGTTGGAGGAGTTAATACCT 180
Qy 236 GTGCATCCAGCAGCGGATTCACCATCTCAAAAACCTGACAAAGACATTTCAAAGAAAGTAT 295
Db 181 GTGCATCCAGCAGCGGATTCACCATCTCAAAAACCTGACAAAGAGTAT 240
Qy 296 TAAATTCATTCAGAGTCCCGGCTCCCGGTGAGAGTGCCTTGTACATGCTCCCTGGCGG 355
Db 241 TAAATTCATTCAGAGTCCCGGCTCCCGGTGAGAGTGCCTTGTACATGCTCCCTGGCGG 300
Qy 356 GGTCTCCAGAGCGTGACACTGGTGATCGCATCATGACCGCTCACTGACTTTGGCTG 415
Db 301 GGTCTCCAGAGCGTGACACTGGTGATCGCATCATGACCGCTCACTGACTTTGGCTG 360
Qy 416 GGAGATGCTCTGCACACCGTGTGCTGGAGATCTCTGTGCCAACCCCAACGTTGGGCTT 475
Db 361 GGAGATGCTCTGCACACCGTGTGCTGGAGATCTCTGTGCCAACCCCAACGTTGGGCTT 420
Qy 476 CCAGAGACAGCTCCAGGAGTTTGAGAGCATAGGTTCCATCAGTATCGGAGTGGCTGAA 535
Db 421 CCAGAGACAGCTCCAGGAGTTTGAGAGCATAGGTTCCATCAGTATCGGAGTGGCTGAA 480
Qy 536 GGAGATATGGAGAGCGCTTTGGAGGATCGAGAGAGCCCAAAACATTTCTGGCGG 595
Db 481 GGAGATATGGAGAGCGCTTTGGAGGATCGAGAGAGCCCAAAACATTTCTGGCGG 540
Qy 596 TCCAGGAATCTGAAGTTCTGGGCTTTCTCAGAAAGACTGTAATGTACCTGAAGTTCTG 655
Db 541 TCCAGGAATCTGAAGTTCTGGGCTTTCTCAGAAAGACTGTAATGTACCTGAAGTTCTG 600
Qy 656 AAATATTGCAAAACCCGAGAGTTTAGCTGTGCTGCAAAAGAAAGCAACATAGT 715
Db 601 AAATATGCAAAACCCCAACAGAGTTTAGCTGTGCTGCAAAAGAAAGCAACATAGT 660

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QY      716 TTAAG 720
Db      661 TTAAG 665

RESULT 10
AV764304
LOCUS   AV764304 MDS Homo sapiens cDNA clone MDSBFH09 5', mRNA linear EST 19-OCT-2000
DEFINITION AV764304
ACCESSION AV764304
VERSION AV764304.1 GI:10922152
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 694)
Gu,J., Zhao,M., Huang,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
Homo sapiens cDNA MDS clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
location/Qualifiers
1..694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MDSBFH09"
/tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="MDS"
/notes="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN
Query Match 69.6%; Score 644.2; DB 1; Length 694;
Best Local Similarity 96.3%; Pred. No. 3.5e-177;
Matches 658; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY      48 ACACGGCCGGGCGTAGCGTTCCGCTTCAGCCACCATGGGGAATGGATGAACAAGATC 107
Db      1 ACACGGCCGGGCGTAGCGTTCCGCTTCAGCCACCATGGGGAATGGATGAACAAGATC 60

QY      108 CTGCCCGGCGCTGTACATCGGCAACTTTCAAAGATGCCAGACGGGGAACAATTGAGCAAG 167
Db      61 CTGCCCGGCGCTGTACATCGGCAACTTTCAAAGATGCCAGACGGGGAACAATTGAGCAAG 120

QY      168 AACAGAGTGACACATATTCTGTCTGTCCACGATAGTCCAGGCCCTATGTTGGAGGGAGTT 227
Db      121 AACAGAGTGACACATATTCTGTCTGTCCACGATAGTCCAGGCCCTATGTTGGAGGGAGTT 180

QY      228 AATAACCTGTGATCCCGACGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 287
Db      181 AATAACCTGTGATCCCGACGCGGATTCACCATCTCAAAACCTGACAGACATTTCAA 240

QY      288 GAAAGTATTAATTCATTTCACGAGTGGCGGTCCCGGTGAGAGCTGCTTGTGACATGC 347
Db      241 GAAAGTATTAATTCATTTCACGAGTGGCGGTCCCGGTGAGAGCTGCTTGTGACATGC 300

QY      348 CTGGCCGGGGTCTCCAGAGCGGTGACATCTGGTGATTCGCATACATGACCGCTCACTGC 407
Db      301 CTGGCCGGGGTCTCCAGAGCGGTGACATCTGGTGATTCGCATACATGACCGCTCACTGC 360

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QY      408 TTTGGCTGGGAGGATGCCCTGTCACACCGTGCCTGGGAGATCCTCTGTGCCAACCCCAAC 467
Db      361 TTTGGCTGNGAGGATGCCCTGTCACACCGTGCCTGGGAGATCCTCTGTGCCAACCCCAAC 420

QY      468 GTGGGCTTCCAGAGACAGACTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGGCAG 527
Db      421 GTGGGCTTCCAGAGACAGACTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGGCAG 480

QY      528 TGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGAGAGATGAGGTCCATCAGTATCGGCAG 587
Db      481 TGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGAGAGATGAGGTCCATCAGTATCGGCAG 540

QY      588 CTGGCCGCTCCAGCAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGACCTGA 647
Db      541 CTGGCCGCTCCAGCAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGACCTGA 600

QY      648 AGTTTCTGAAATATATGCAAAACCCGACAGTTTAGGCTGTGCTGCCAAAAGAAAAGCAA 707
Db      601 AGTTTCTGAAATATATGCAAAACCCGACAGTTTAGGCTGTGCTGCCAAAAGAAAAGCAA 660

QY      708 CATAGAGTTTAAGTATCCAGTAG 730
Db      661 GAGTTTGTATCAGTAGTAGTTG 683

RESULT 11
CD693732
LOCUS   EST10255 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
DEFINITION CD693732
ACCESSION CD693732
VERSION CD693732.1 GI:32217678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 655)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 67.2%; Score 622.4; DB 6; Length 655;
Best Local Similarity 99.8%; Pred. No. 8.6e-171;
Matches 623; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      77 AGCCACCATGGGAATGGGATGAACAAGATCCTGCCCGGCTGTACATCGGCAACTTCAA 136
Db      32 AGCCACCATGGGAATGGGATGAACAAGATCCTGCCCGGCTGTACATCGGCAACTTCAA 91

QY      137 AGATGCCAGAGACCGGGAACAATTTGACCAAGAACAGGTGACACATATTTCTGTCTGCCA 196
Db      92 AGATGCCAGAGACCGGGAACAATTTGACCAAGAACAGGTGACACATATTTCTGTCTGCCA 151

QY      197 CGATAGTGCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGATCCAGCAGCGGATTC 256

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Db 152 CGATAGTCCAGGCGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 211
QY 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316
Db 212 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 271
QY 317 GCTCCGCGGTGAGAGTGCCTTTGACACTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 376
Db 272 GCTCCGCGGTGAGAGTGCCTTTGACACTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 331
QY 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGATGCCCTGCACACGT 436
Db 332 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGATGCCCTGCACACGT 391
QY 437 GCGTGTGGGAGATCCTGTGTCCAAACCCCAACCTGGGCTTCCAGAGACAGCTCCAGGAGTT 496
Db 392 GCGTGTGGGAGATCCTGTGTCCAAACCCCAACCTGGGCTTCCAGAGACAGCTCCAGGAGTT 451
QY 497 TGAGAAGCATGAGTCCATCATGATTCGCGAGTGGCTGAAGGAAGATATGGAGAGAGCCC 556
Db 452 TGAGAAGCATGAGTCCATCATGATTCGCGAGTGGCTGAAGGAAGATATGGAGAGAGCCC 511
QY 557 TTTGAGAGTGCAGAGAGCCAAACATTTCTGCGCGCTCCAGGAATTTCTGAAGTTCTG 616
Db 512 TTTGAGAGTGCAGAGAGCCAAACATTTCTGCGCGCTCCAGGAATTTCTGAAGTTCTG 571
QY 617 GGCCTTTCTCAGAGACTGTAATCTGACTGAAGTTTCTGAAATATTCGAACCCGAGAG 676
Db 572 GGCCTTTCTCAGAGACTGTAATCTGACTGAAGTTTCTGAAATATTCGAACCCGAGAG 631
QY 677 TTTAGGCTGGTGTGCCAAAAGA 700
Db 632 TTTAGGCTGGTGTGCCAAAAGA 655

RESULT 12
CB995799 819 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT_13684680 NIH_MGC_148 Homo sapiens cDNA clone
DEFINITION IMAGE:30332322 5', mRNA sequence.
CB995799
VERSION CB995799.1 GI:30290223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM349 row: c column: 19
High quality sequence stop: 528.
Location/Qualifiers
1. 819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30332322"
/tissue_type="pre-eclampsia placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
source

all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTN-3', size-selected for average insert
size 2.3 kb and normalized to 50x. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 65.6%; Score 607; DB 6; Length 819;
Best Local Similarity 96.7%; Pred. No. 3e-166;
Matches 641; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
QY 42 GCGACACACAGCGCGCGCTAGCGTTCCGCTTCAGCCACCATGGGGAATGGATGAAC 101
Db 5 GCGAGTGACAGCGGTAGAACCCAGCGTTCCGCTTCAGCCACCATGGGGAATGGATGAAC 64
QY 102 AAGATCTGCGCGCGCTGTACATCGGCAACTTCAAAGATCCAGAGAGCGCGGAACAATTG 161
Db 65 AAGATCTGCGCGCGCTGTACATCGGCAACTTCAAAGATCCAGAGAGCGCGGAACAATTG 124
QY 162 AGCAAGAAACAAGGTGACACATATTTCTGTCTCCACGATAGTCCAGGCTTATGTTGAG 221
Db 125 AGCAAGAAACAAGGTGACACATATTTCTGTCTCCACGATAGTCCAGGCTTATGTTGAG 184
QY 222 GGAGTTAAATACCTGTCATCCAGAGAGCGGATTCACCAATCTCAAAACCTGACAGACAT 281
Db 185 GGAGTTAAATACCTGTCATCCAGAGAGCGGATTCACCAATCTCAAAACCTGACAGACAT 244
QY 282 TTCAGAAAGAGTATTAATTCATTACAGAGTCCCGGCTCCGCGGTGAGAGCTGCTTGTGA 341
Db 245 TTCAGAAAGAGTATTAATTCATTACAGAGTCCCGGCTCCGCGGTGAGAGCTGCTTGTGA 304
QY 342 CACTGCTGCGCGGGGTCTCCAGAGAGCGTGA CACTGCTGATCGCATACATCATGACCGTC 401
Db 305 CACTGCTGCGCGGGGTCTCCAGAGAGCGTGA CACTGCTGATCGCATACATCATGACCGTC 364
QY 402 ACTGACTTTGGCTGGGAGAGTCCCTGCACACCGTGGCTGGGAGATCTCTGTCGCAAC 461
Db 365 ACTGACTTTGGCTGGGAGAGTCCCTGCACACCGTGGCTGGGAGATCTCTGTCGCAAC 423
QY 462 CCACAGTGGCTTCCAGAGAGAGCTCCAGAGAGTTCAGAGAGTTCAGAGAGTTCAGAT 521
Db 424 CCACAGTGGCTTCCAGAGAGAGCTCCAGAGAGTTCAGAGAGTTCAGAT 483
QY 522 CGCAGTGGCTGAAGGAAGATATGGAGAGAGCGCTTTTCAGAGATGAGAGAGAGAGAG 581
Db 484 CGCAGTGGCTGAAGGAAGATATGGAGAGAGCGCTTTTCAGAGATGAGAGAGAGAGAG 543
QY 582 AACATCTGCGCGCTCCAGGAATTCAGAGTTCGGGCTTTCTCAGAGAGTCTGATATGT 641
Db 544 AACATCTGCGCGCTCCAGGAATTCAGAGTTCGGGCTTTCTCAGAGAGTCTGATATGT 603
QY 642 ACCT-GAAGTTTCTGAATATTCGAACCCGAGAGTTTAGGCTGGTGGTGGTGGTGGT 700
Db 604 ACCTGAAGTTTCTGAATATTCGAACCCGAGAGTTTAGGCTGGTGGTGGTGGTGGT 663
QY 701 AAA 703
Db 664 AAA 666

RESULT 13
CA453928
LOCUS AGENCOURT_10739523 MAPcL Homo sapiens cDNA clone IMAGE:6718575 5',
DEFINITION mRNA sequence.
CA453928
ACCESSION CA453928.1 GI:24903167
VERSION CA453928.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 930)
 NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M14275 row: b column: 15
 High quality sequence stop: 658.
 FEATURES
 source Location/Qualifiers
 1..930
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IWAGS:6718575"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 hTERT-HME1, LNCaP"
 /lab_host="EMDH10B"
 /clone_lib="MAPCL"
 /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bungkook Lee & Ira Pastan. Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."
 ORIGIN
 Query Match 62.9%; Score 582.4; DB 6; Length 930;
 Best Local Similarity 93.8%; Pred. No. 5.1e-159;
 Matches 640; Conservative 0; Mismatches 36; Indels 6; Gaps 3;
 QY 80 CACATCGGGAATGGATGACAGATCTCGCGGCTGTACATCGGCACTTCAAAGA 139
 DB 191 CGCGTGGCCATGTGACGCGCTACATCTCGCGGCTGTACATCGGCACTTCAAAGA 250
 QY 140 TGGCAGAGCGCGAACAATTTGAGCAAGAAACAAGGTGACACATATCTGTCTGCCACGA 199
 DB 251 TGGCAGAGCGCGAACAATTTGAGCAAGAAACAAGGTGACACATATCTGTCTGCCACGA 310
 QY 200 TAGTCCAGCGCTATGTTGGAGGAGTTAAATACCTGTGATCCAGCAGCGGATTCACC 259
 DB 311 TAGTCCAGCGCTATGTTGGAGGAGTTAAATACCTGTGATCCAGCAGCGGATTCACC 370
 QY 260 ATCTCAAACTGACAGACATTTCAAGAAAGTATTAATTCATTCACGAGTCCGGCT 319
 DB 371 ATCTCAAACTGACAGACATTTCAAGAAAGTATTAATTCATTCACGAGTCCGGCT 430
 QY 320 CCGCGGTGAGAGTGCCTTGTACACTGCTGCGCGGCTTCCAGGAGCGTGACACTGGT 379
 DB 431 CCGCGGTGAGAGTGCCTTGTACACTGCTGCGCGGCTTCCAGGAGCGTGACACTGGT 490
 QY 380 GATGCGCATACATGACCGTCACTGATTTGGCTGGAGAGATGCCCTGCACACCGGTGG 439
 DB 491 GATGCGCATACATGACCGTCACTGATTTGGCTGGAGAGATGCCCTGCACACCGGTGG 550
 QY 440 TGCTGGGAGATCTGTGCGCAACCCACGCTGGCTCCAGAGACAGCTCCAGAGTTGA 499
 DB 551 TGCTGGGAGATCTGTGCGCAACCCACGCTGGCTCCAGAGACAGCTCCAGAGTTGA 610
 QY 500 GAAGCATGAGGTCCATCAGTATCGGCACTGGCTGAAGAAAGATATATGAGAGAGCCCTTT 559
 DB 611 GAAGCATGAGGTCCATCAGTATCGGCACTGGCTGAAGAAAGATATATGAGAGAGCCCTTT 670

QY 560 GCAGGATGCAAGAGAGCCAAACAACTTCTGGCCGCTCAGGAATTTCTGAAGTCTGGG- 618
 DB 671 GCAGGATGCAAGAGAGCCAAACAACTTCTGGCCGCTCAGGAATTTCTGAAGTCTGGG- 730
 QY 619 CTTTCTCAGAAGACTGTATGTACCTGAAGTCTTCTGAATATTTGCAAACTTCCAGAGTT 678
 DB 731 CTTTCTCAGAAGACTGTATGTACCTGAAGTCTTCTGAATATTTGCAAACTTCCAGAGTT 790
 QY 679 TAGGCTGGTG-CTGCCAAAGAAAGCAACATAGAGTTTAA---GTATCCAGTAGTGA 733
 DB 791 TAAGCTGGTGCTGCCAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGA 850
 QY 734 TTGTAAACTTGTGTTTTCATT 755
 DB 851 TTGCTAAACTTGTGTTTTCATT 872
 RESULT 14
 BG545679 751 bp mRNA linear EST 04-APR-2001
 LOCUS 602572945F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701034 5',
 DEFINITION mRNA sequence.
 ACCESSION BG545679.1 GI:13544344
 VERSION BG545679
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 751)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M1535 row: j column: 11
 High quality sequence stop: 680.
 FEATURES
 source Location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4701034"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgctcgcc); Site 2: SfiI (ggcgatattggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGCGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 61.5%; Score 569.4; DB 4; Length 751;
 Best Local Similarity 99.7%; Pred. No. 3.1e-155;
 Matches 581; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 10 TCCTCTCTCCCTGTAACATGCTAGTGGCTCGGACCAACACGCGCGGCGCTAGCGTT 69
 DB 2 TCCTCTCTCCCTGTAACATGCTAGTGGCTCGGACCAACACGCGCGGCGCTAGCGTT 61

QY 70 CGCCTTCAGCCACCACCATGGGATGGGATGAACAAGATCCTGCCCGGCTGTACATCGGCA 129
Db 62 CGCCTTCAGCCACCACCATGGGATGGGATGAACAAGATCCTGCCCGGCTGTACATCGGCA 121
QY 130 ACTTCAAG-ATGCAGAGAGCGGGAACAATTGAGCAAGAACAAAGGTGACACATATTTCTG 188
Db 122 ACTTCAAGATATGCAGAGAGCGGGAACAATTGAGCAAGAACAAAGGTGACACATATTTCTG 181
QY 189 TCTGTCCACCATAGTGCAGGCTTATGTTGGAGGAGTTAAATACCTGTGTGATCCAGCA 248
Db 182 TCTGTCCACCATAGTGCAGGCTTATGTTGGAGGAGTTAAATACCTGTGTGATCCAGCA 241
QY 249 GCGGATTCACCATCTCAAACTGACAAGACATTTCAAGAAAGTATTAATTCATTCAC 308
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Db 542 GAGAGCCCTTTGAGGATGAGAGAGAGCCAAACCAATTCCTGG 584

RESULT 15

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LOCUS 170006001.86907 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
CN394735
VERSION CN394735.1 GI:47382330
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.

TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation

JOURNAL

COMMENT Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

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Location/Qualifiers

1..712

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/tissue_type="embryonic stem cell, retinoic acid and

mitogen-treated hES cell line H7"

/clone_lib="GRN_PRENEU"

/note="oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free

conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."

ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 3e-154;

Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCCATAGTGGCTTCGCGACCAACACGCGCGGGCGCTAGCGTTTCGGCTTCAGCCACCAT 60

QY 86 GGGGAATGGGATGAACAAGATCTGCGCCGCCCTGTATCATCGGCAATTTCAAAGATGCCAG 145

Db 61 GGGGAATGGGATGAACAAGATCTGCGCCGCCCTGTATCATCGGCAATTTCAAAGATGCCAG 120

QY 146 AGACGGGAACAATTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATAGTGC 205

Db 121 AGACGGGAACAATTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATAGTGC 180

QY 206 CAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 265

Db 181 CAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 240

QY 266 AAACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTCACGAGTCCCGGCTCCCGG 325

Db 241 AAACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTCACGAGTCCCGGCTCCCGG 300

QY 326 TGAGAGTGCCTTGTATACACTGCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGC 385

Db 301 TGAGAGTGCCTTGTATACACTGCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGC 360

QY 386 ATACATCATGACCGTCACTGACTTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGG 445

Db 361 ATACATCATGACCGTCACTGACTTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGG 420

QY 446 GAGATCCTGTGCCAACCCCAACGTTGCCAGAGACAGTCCAGGAGTTTGAGAAGCA 505

Db 421 GAGATCCTGTGCCAACCCCAACGTTGCCAGAGACAGTCCAGGAGTTTGAGAAGCA 480

QY 506 TGAGGTTCCATCAGTATCGGAGTGGCTGAAGGAAGAAATATGGAGAGCCCTTTGCAGGA 565

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)

8942.383 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	926	100.0	926	4	AAF29601 Human DSP
2	926	100.0	926	4	Aaf32191 Human dua
3	926	100.0	926	10	ACC69509 Human DSP
4	926	100.0	926	12	ADN75953 Human sig
C 5	924	99.8	1187	4	AAS41391
C 6	924	99.8	1187	4	AAS41395
C 7	924	99.8	1187	10	ADC46153
8	923.6	99.7	1187	6	ABL90844 Human pol
9	922.8	99.7	1379	4	AAF63568 Human pho
10	922.8	99.7	1520	8	ACC83479 Human mit
11	922.8	99.7	1520	10	ADD89786 Human MKP
12	922.8	99.7	1520	13	ADP25000 PRO polyp
13	921.2	99.5	1290	3	AAZ46164 cDNA sequ
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16	875.8	94.6	910	4	AAS34867 cDNA enco
17	875.8	94.6	910	10	ADC46025 Human neo
18	800.8	86.5	875	3	AAC63800 Human dua
19	623.4	67.3	625	4	AA164795 Human MAP
20	589.4	63.7	1218	5	AAF86152 Human JNK

21	563.2	60.8	1067	4	AAF63565	Aaf63565 Murine ph
22	555	59.9	555	4	AAF29612	Aaf29612 Human DSP
23	488	52.7	2835	10	ADB63347	Adb63347 Human cDN
24	479.6	51.8	2735	4	AAS41048	Aas41048 cDNA enco
25	469.2	50.7	2368	4	AAS41588	Aas41588 cDNA enco
26	421.2	45.5	687	4	AAF29608	Aaf29608 Murine DS
27	418.6	45.2	3010	5	AAF86153	Aaf86153 Murine JN
28	375.4	40.5	2420	6	ABZ35370	Abz35370 Human gen
29	334.4	36.1	3824	13	ADR06882	Adr06882 Full leng
30	274.2	29.6	555	12	ACH76515	Ach76515 Human gen
31	270.4	29.2	279	6	ABL70917	Ab170917 Corn tab88
32	200.8	21.7	867	10	ACC69512	Acc69512 Human DSP
33	200.8	21.7	1160	6	AAD36481	Aad36481 Human pro
34	200.8	21.7	1160	10	ACC69513	Acc69513 Human DSP
35	199.2	21.5	833	10	ACC69495	Acc69495 Human dua
36	199.2	21.5	833	12	ADN75957	Adn75957 Human sig
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38	199.2	21.5	1325	6	ABK14477	Abk14477 Human pro
39	199.2	21.5	1326	4	AAD09498	Aad09498 Human SGP
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44	191.2	20.6	289	3	AAC75779	Aac75779 Human ORF
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ALIGNMENTS

RESULT 1

AAF29601 AAF29601 standard; cDNA; 926 BP.

XX AAF29601;

DT 06-APR-2001 (first entry)

XX Human DSP-3 CDNA.

XX Human; DSP-3; cytostatic; immunosuppressive; anti-allergic;

KW dual specificity phosphatase-3; cell proliferation; metabolic diseases;

KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;

KW autoimmune disease; allergy; ss.

XX Homo sapiens.

XX WO200102582-A1.

XX 11-JAN-2001.

PD 29-JUN-2000; 2000WO-US018207.

XX 02-JUL-1999; 99US-0142338P.

PR 07-APR-2000; 2000WO-US009185.

PR 20-APR-2000; 2000WO-US010868.

XX (CBPT-) CBPTYR INC.

XX Luche RM, Wei B;

XX WPI; 2001-138149/14.

XX P-FSDB; AAB66431.

XX New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form

PT polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate

PT form activity, especially for treating e.g. cancer, autoimmune diseases

PT or allergies.

XX Claim 7; Fig 1; 86pp; English.

XX The present sequence is given in a specification providing human dual

CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.

CC The polypeptides are useful for dephosphorylating a substrate of DSP-3,
 CC e.g. MAP-kinase. They may be used to treat or prevent diseases associated
 CC with cell proliferation, immunosuppression, metabolic diseases, or
 CC abnormal cell growth or cell cycle abnormalities. They are also useful
 CC for identifying agents that modulate their activity. The modulators are
 CC useful for treating disorders associated with DSP-3 or DSP-3 variant
 CC activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
 CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal
 CC cell growth, abnormal cell proliferation and cell cycle abnormalities.
 CC The modulating agents are useful for modulating, modifying or altering
 CC cellular responses, e.g. in vivo or in vitro cell proliferation,
 CC differentiation or survival
 XX
 SQ Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 926; DB 4; Length 926;
 Best Local Similarity 100.0%; Pred. No. 1.1e-263;
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 ID AAF32191 standard; cDNA; 926 BP.
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 AC AAF32191;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Human dual-specificity phosphatase DSP-3 coding sequence.
 XX
 KW Human; DSP-3; dual-specificity phosphatase; cell proliferation;
 KW cell signalling; cancer; graft-versus-host disease; autoimmune disease;
 KW allergy; metabolic disease; Duchenne muscular dystrophy; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200102581-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 20-APR-2000; 2000WO-US010868.
 XX
 PR 02-JUL-1999; 99US-0142338P.
 PR 07-APR-2000; 2000WO-US009185.
 XX
 PA (CEPT-) CEPTYR INC.
 XX
 PI Luche RM, Wei B;
 XX
 DR WPI; 2001-138148/14.
 DR P-PSDB; AAB67167.
 XX
 PT New dual-specificity phosphatase-3 polypeptide and its variants useful
 PT for treating disorders associated with DSP-3 activity, defects in cell
 PT proliferation, differentiation or survival, e.g. Duchenne muscular
 PT dystrophy, cancer.
 XX
 PS Claim 7; Fig 1; 70pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human dual-specificity phosphatase DSP-3. The DSP-3 protein is involved
 CC in cell signalling and the sequences can be used in the treatment of
 CC cancer, metabolic and autoimmune diseases, allergies, graft-versus-host
 CC disease, abnormal cell proliferation and Duchenne muscular dystrophy
 XX
 SQ Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 926; DB 4; Length 926;
 Best Local Similarity 100.0%; Pred. No. 1.1e-263;
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 ATATTCTGTCTCCACGATAGTGCAGGCCCTATGTTGGAGGAGTTAAATPACCTGTGCA 240
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 Qy 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAAT 300
 Db 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAAT 300
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 Db 301 TCATTTCAGAGTGCCTGCTCCGCGTGGAGCTGCTGTTGATACCTGCTGCGCGGGTCT 360
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 Db 361 CCAGAGCGTGCACACTGCTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
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 Db 421 ATGCCCTGCACACGTCGCTGCTGGAGATCTGTCGCAACCCCAACGTCGGCTTCAGA 480
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 Db 721 TATCCAGTAGTGATTTGAACCTTTGTTTTCATTTGAAGCTGGAATATATAGTAGTCATG 780
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 Db 781 TTTATGTTGAGAACTAAGATATTTCTTTAGCAAGAGAAATATTTTCCCTTATCCCAAC 840
 Qy 841 TGCTGTGGAGGTTTCTGACCTGCTGGATGCTGTAAGATCCCGGAGCCTTGGCGC 900
 Db 841 TGCTGTGGAGGTTTCTGACCTGCTGGATGCTGTAAGATCCCGGAGCCTTGGCGC 900
 Qy 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
 Db 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
 RESULT 3
 ID ACC69509
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 XX ACC69509;
 XX 21-JUL-2003 (first entry)
 XX Human DSP-3 polynucleotide sequence SEQ ID NO:34.
 KW Human; dual-specificity phosphatase; DSP-18; enzyme; cytostatic;
 KW immunosuppressive; antiallergic; MAP-kinase modulator; dephosphorylation;
 KW signal transduction modulator; cell proliferation; cell differentiation;
 KW cell survival; proliferative response; Duchenne muscular dystrophy;
 KW cancer; graft-versus-host disease; autoimmune disease; allergy;
 KW metabolic disease; abnormal cell growth; abnormal cell proliferation;
 KW cell cycle abnormality; gene; ss.
 OS Homo sapiens.

XX WO2003025196-A2.
 XX 27-MAR-2003.
 XX 16-MAY-2002; 2002WO-US015906.
 XX 16-MAY-2001; 2001US-0291476P.
 XX (CBPT-) CBPTV INC.
 XX Luche RM, Wei B;
 XX WPI; 2003-371819/35.
 XX New DSP-18 dual-specificity phosphatases, useful for modulating cell
 XX proliferation, differentiation or survival, or for identifying modulators
 XX of DSP-18 activity for treating e.g. cancer or graft-versus-host disease
 XX in a patient.
 XX Example 5; Page 109-110; 113pp; English.
 XX ACC69489 to ACC69495 encode the human dual-specificity phosphatases
 XX designated DSP-18a to DSP-19f and prototypical DSP-18pr given in ABR43450
 XX to ABR43456. DSP-18 proteins have the ability to dephosphorylate an
 XX activated mitogen activated protein (MAP)-kinase. DSP-18 sequences have
 XX cytosolic, immunosuppressive and antiallergic activities, and can be
 XX used as modulators of MAP-kinases and signal transduction. The DSP-18
 XX proteins can be used for identifying antibodies and other modulators
 XX (particularly inhibitors) of DSP-18 activity. The DSP-18 proteins may be
 XX used to modulate cell proliferation, cell differentiation and cell
 XX survival, or to treat diseases associated with cell proliferation,
 XX differentiation or survival. The DSP-18 proteins are especially useful
 XX for stimulating dephosphorylation of DSP-18 substrates. A modulator of
 XX DSP-18 activity can be used for modulating a proliferative response in a
 XX cell, differentiation of a cell or survival of a cell; or for treating a
 XX patient afflicted with a disorder (e.g. Duchenne muscular dystrophy,
 XX cancer, graft-versus-host disease, autoimmune diseases, allergies,
 XX metabolic diseases, abnormal cell growth, abnormal cell proliferation, or
 XX cell cycle abnormalities) associated with DSP-18 activity. The present
 XX sequence represents a human DSP-3 polynucleotide sequence which is used
 XX in an example from the present invention
 XX SQ Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 U; 0 Other;
 Query Match 100.0%; Score 926; DB 10; Length 926;
 Best Local Similarity 100.0%; Pred. No. 1.1e-263; Indels 0; Gaps 0;
 Matches 926; Conservative 0; Mismatches 0;
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 Db 1 CCCCGCGCTCCTCCTCCCTGTAACATGCGCATAGTGGCCCTGCCACACACGCGCGGGC 60
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 Db 61 GCTAGCGTTCCCTTCAGCCACCATGCGGGAATGGGATGAACAAGATCCTGCGCGCTGT 120
 Qy 121 ACATCGGCAACTTCAAGATGCCAGAGACCGGGAACAAATTGAGCAAGAACAGGTGACAC 180
 Db 121 ACATCGGCAACTTCAAGATGCCAGAGACCGGGAACAAATTGAGCAAGAACAGGTGACAC 180
 Qy 181 ATATTCTGTCTGCTCCAGATAGTCCAGGCTATGTTGGAGGAGTTAAATPACCTGTGCA 240
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 Qy 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAAT 300
 Db 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAAT 300
 Qy 301 TCATTTCAGAGTGCCTGCTCCGCGTGGAGCTGCTGTTGATACCTGCTGCGCGGGTCT 360
 Db 301 TCATTTCAGAGTGCCTGCTCCGCGTGGAGCTGCTGTTGATACCTGCTGCGCGGGTCT 360

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 421 ATGCCCTGCACACCGCTGGTGTGGAGATCTGTGCCAACCCCAACGCTGGGCTTCCAGA 480
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 601 GAATTTCTGAAGTTCTGGGCCCTTCTCAGAGACTGTATGTACCTGAAAGTTTCTGAATA 660
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 661 TTGCAAAACCCGAGTTTGGCTGGTGTCTGCCAAAAGAAAGCAACATAGATTTTAAG 720
 661 TTGCAAAACCCGAGTTTGGCTGGTGTCTGCCAAAAGAAAGCAACATAGATTTTAAG 720
 721 TATCAGTAGTGAATTTGAACTTTTTCATTTGAGCTGAATATATAGTATCATG 780
 721 TATCAGTAGTGAATTTGAACTTTTTCATTTGAGCTGAATATATAGTATCATG 780
 781 TTTATGTTGAGAACTAAGATATTTTTCAGAGAGAAATATTTTCCCTTTATCCCCAC 840
 781 TTTATGTTGAGAACTAAGATATTTTTCAGAGAGAAATATTTTCCCTTTATCCCCAC 840
 841 TGCTGTGAGAGTTTCTGATCTGCTGAGTGTGATGCTGTGAAGATCCCGGAGCCCTTGGCG 900
 841 TGCTGTGAGAGTTTCTGATCTGCTGAGTGTGATGCTGTGAAGATCCCGGAGCCCTTGGCG 900
 901 ACTGCTGTGGGTGGCTTGGCGCTC 926
 901 ACTGCTGTGGGTGGCTTGGCGCTC 926

RESULT 4
 ADN75953
 ID ADN75953 standard; DNA; 926 BP.
 AC ADN75953;
 XX
 XX
 DT 01-JUL-2004 (first entry)
 XX Human signal transduction-associated DNA SEQ ID 778.
 DE
 XX small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
 KW cytoskeletal; immunomodulator; antimicrobial; anti-inflammatory;
 KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
 KW inflammation; diabetes; obesity; RNA interference; gene silencing; ds;
 KW gene.

OS Homo sapiens.
 XX WO2004016735-A2.
 XX
 XX 26-FEB-2004.
 XX
 XX 23-MAY-2003; 2003WO-US016632.
 XX
 XX 23-MAY-2002; 2002US-0383249P.
 XX
 XX 14-APR-2003; 2003US-0462942P.
 XX
 XX (CEPT-) CEPTV INC.
 XX (COLD-) COLD SPRING HARBOR LAB.
 XX
 XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;

DR WPI; 2004-203773/19.
 DR P-PSDB; ADN75954.
 XX
 PT New isolated small interfering RNA (siRNA) polynucleotide useful for
 PT treating diseases with aberrant activity of the protein tyrosine
 PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
 PT diabetes and obesity.
 XX
 PS Disclosure; SEQ ID NO 778; 392pp; English.
 XX
 CC This invention describes novel small interfering RNA (siRNA)
 CC polynucleotides capable of interfering with expression of a polypeptide
 CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
 CC invention have cytoskeletal, immunomodulator, antimicrobial,
 CC anti-inflammatory, antidiabetic and anorectic activity. The methods and
 CC compositions of the present invention are useful for treating diseases or
 CC conditions associated with aberrant expression or activity of the protein
 CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
 CC inflammation, diabetes and obesity. This sequence represents a siRNA
 CC directed against dual specificity phosphatase (DSP) expression.
 XX
 SQ Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 926; DB 12; Length 926;
 Best Local Similarity 100.0%; Pred. No. 1.1e-263;
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCCGCGCTCCTCCTCCCTGTAACATGTCATGTCGCTGCCACACACGCGCGGGC 60
 Db 1 CCCCGCGCTCCTCCTCCCTGTAACATGTCATGTCGCTGCCACACACGCGCGGGC 60
 Qy 61 GCTAGCTTGCCTTCAGCCACCATGCGGAATGGGATGAACAAGATCCTGCCCGGCTGT 120
 Db 61 GCTAGCTTGCCTTCAGCCACCATGCGGAATGGGATGAACAAGATCCTGCCCGGCTGT 120
 Qy 121 ACATCGGCAACTTCAAGATGCCAGACGCGGAACAATTTGAGCAAGAACAAAGGTGACAC 180
 Db 121 ACATCGGCAACTTCAAGATGCCAGACGCGGAACAATTTGAGCAAGAACAAAGGTGACAC 180
 Qy 181 ATATTTCTGTCTGCACGATAGTCCAGGCTTATGTTGGAGGGAGTTAAATACCTGTGCA 240
 Db 181 ATATTTCTGTCTGCACGATAGTCCAGGCTTATGTTGGAGGGAGTTAAATACCTGTGCA 240
 Qy 241 TCCAGAGCGGATTCACATCTCAAAACCTGACACACATTTCAAAGAAGTTTAAAT 300
 Db 241 TCCAGAGCGGATTCACATCTCAAAACCTGACACACATTTCAAAGAAGTTTAAAT 300
 Qy 301 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGTCCCTTGTACACTGCTGCCGCGGTCT 360
 Db 301 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGTCCCTTGTACACTGCTGCCGCGGTCT 360
 Qy 361 CCAGGAGCGTGACACTGGTGTATGCATATCATGACCGTCACTGACTTTGGCTGGGAGG 420
 Db 361 CCAGGAGCGTGACACTGGTGTATGCATATCATGACCGTCACTGACTTTGGCTGGGAGG 420
 Qy 421 ATGCCCTGCACACCGTGGCTGTGGAGATCTGTGCCAACCCCAACGCTGGGCTTCCAGA 480
 Db 421 ATGCCCTGCACACCGTGGCTGTGGAGATCTGTGCCAACCCCAACGCTGGGCTTCCAGA 480
 Qy 481 GACAGCTCCAGGAGTTTGAAGATCATGAGTCCATCATGATCGGAGTGGCTGAAGGAAG 540
 Db 481 GACAGCTCCAGGAGTTTGAAGATCATGAGTCCATCATGATCGGAGTGGCTGAAGGAAG 540
 Qy 541 AATATGAGAGAGCCCTTTTCAGAGATCGAGAAGAGCCAAACATTTCTGGCCGCTCCAG 600
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 Qy 601 GAATTTCTGAAGTTCTGGGCCCTTCTCAGAGACTGTATGTACCTGAAAGTTTCTGAATA 660
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 Qy 661 TTGCAAAACCCGAGTTTGGCTGGTGTCTGCCAAAAGAAAGCAACATAGATTTTAAG 720

Db 661 TTGCAAAACCCGACAGTTTAGCTGGTCTGCCAAAAAGAAAGCAACATAGAGTTTAAAG 720
QY 721 TATCCAGTAGTGAATTTGAAACTTCTTTTTCATTGGAAGCTGAATATATACGTAGTCAAG 780
Db 721 TATCCAGTAGTGAATTTGAAACTTCTTTTTCATTGGAAGCTGAATATATACGTAGTCAAG 780
QY 781 TTTATGTTGAGAACTAAGGATATCTTTTACGAAGAGAAAAATTTTCCCTTATCCCCAC 840
Db 781 TTTATGTTGAGAACTAAGGATATCTTTTACGAAGAGAAAAATTTTCCCTTATCCCCAC 840
QY 841 TGCTGTGAGCTTTCTGTACCTCGCTTGGATCCCTGTAAGGATCCCGGAGCCTTGCGGC 900
Db 841 TGCTGTGAGCTTTCTGTACCTCGCTTGGATCCCTGTAAGGATCCCGGAGCCTTGCGGC 900
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Db 901 ACTGCTTGTGGGTGGCTTGGCGCTC 926

RESULT 5
ID AAS41391/c
XX AAS41391 standard; cDNA; 1187 BP.
AC AAS41391;
XX
DT 17-DEC-2001 (first entry)
XX
DE cDNA encoding novel human enzyme polypeptide #607.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ss.
XX
OS Homo sapiens.
XX
FN WO200155301-A2.
XX
PD 02-AUG-2001.
XX
PP 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 11-JUL-2000; 2000US-0217487P.
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PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225758P.

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18-AUG-2000; 2000US-0226279P.
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06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231242P.
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08-SEP-2000; 2000US-0232081P.
12-SEP-2000; 2000US-0231968P.
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14-SEP-2000; 2000US-0232398P.
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14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
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14-SEP-2000; 2000US-0233064P.
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21-SEP-2000; 2000US-0234223P.
21-SEP-2000; 2000US-0234274P.
25-SEP-2000; 2000US-0234997P.
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26-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
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29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
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02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
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20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251988P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
FI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465566/50.
DR P-PSDB; AAU23521.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
PS Claim 4; SEQ ID NO 617; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AA540785-AA541684 represent
CC cDNA sequences encoding for the novel human enzyme polypeptides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1187 BP; 288 A; 302 C; 290 G; 306 T; 0 U; 1 Other;

Query Match 99.8%; Score 924; DB 4; Length 1187;
Best Local Similarity 99.8%; Pred. No. 5e-263;
Matches 924; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGCGCGCTCCTCCTCCTGTAACATGCCATAGTGGCGCTGGACACACACGCGCGGGC 60
Db |||||
1156 CCGCGCGCTCCTCCTCCTGTAACATGCCATAGTGGCGCTGGACACACACGCGCGGGC 1097
Qy 61 GCTAGCGTTGCGCTTTCAGCCACCATGGGAATGGGATGAACAAGATCCTGCGCGCGCTGT 120
Db |||||
1096 GCTAGCGTTGCGCTTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCGCGCGCTGT 1037
Qy 121 ACATCGGCAACTTCAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGGTGACAC 180
Db |||||
1036 ACATCGGCAACTTCAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGGTGACAC 977
Qy 181 ATATTCTGTCTGTCCACGATAGTCCAGGCGCTATTTGGAGGGAGTTAAATACCTGTGCA 240
Db |||||
976 ATATTCTGTCTGTCCACGATAGTCCAGGCGCTATTTGGAGGGAGTTAAATACCTGTGCA 917
Qy 241 TCCAGCAGCGGATTTCAACCATCTCAAAACCTGACAGACATTTCAAAAGAAAGTATTAAAT 300
Db |||||
916 TCCAGCAGCGGATTTCAACCATCTCAAAACCTGACAGACATTTCAAAAGAAAGTATTAAAT 857
Qy 301 TCATTTCAGAGTGC CGGCTCCGCGTGGAGTGCCTTTGTACACTGCTGCGCGGGTCT 360
Db |||||
856 TCATTTCAGAGTGC CGGCTCCGCGTGGAGTGCCTTTGTACACTGCTGCGCGGGTCT 797
Qy 361 CCAGGAGCGTGACACTGGTGTATCGCATACATCATGACCGCTCACTGACTTTGGCTGGGAGG 420
Db |||||
796 CCAGGAGCGTGACACTGGTGTATCGCATACATCATGACCGCTCACTGACTTTGGCTGGGAGG 737
Qy 421 ATGCCCTGCACACCGTCCGCTGGGAGATCCTGTGTGCAACCCCAACCGTGGCTTCCAGA 480
Db |||||
736 ATGCCCTGCACACCGTCCGCTGGGAGATCCTGTGTGCAACCCCAACCGTGGCTTCCAGA 677
Qy 481 GACAGTCCAGGAGTTTGAAGAAGATGAGTGCATCATAGTATCGGCAGTGGCTGAAGGAAG 540
Db |||||
676 GACAGTCCAGGAGTTTGAAGAAGATGAGTGCATCATAGTATCGGCAGTGGCTGAAGGAAG 617
Qy 541 AATATGAGAGAGCGCTTTTCAGGATGCAAGAGCGCAAGAGCCAAACATTTCTGCGCGCTCCAG 600
Db |||||
616 AATATGAGAGAGCGCTTTTCAGGATGCAAGAGCGCAAGAGCCAAACATTTCTGCGCGCTCCAG 557
Qy 601 GAATTCTGAAGTTCTGGGCGCTTTCTCAGAAGACTGTAATGTACCTGAAGTTTCTGAAATA 660
Db |||||
556 GAATTCTGAAGTTCTGGGCGCTTTCTCAGAAGACTGTAATGTACCTGAAGTTTCTGAAATA 497
Qy 661 TTGCAAAACCCGACAGTTTATAGGTGGTGGTGCCTGCAAAAGAAAGCAACATAGAGTTTAAAG 720
Db |||||
496 TTGCAAAACCCGACAGTTTATAGGTGGTGGTGCCTGCAAAAGAAAGCAACATAGAGTTTAAAG 437
Qy 721 TATCCAGTATGATTTGTAACCTTTTTCATTTGAAGCTGAATATATACGTAGTCAATG 780
Db |||||
436 TATCCAGTATGATTTGTAACCTTTTTCATTTGAAGCTGAATATATACGTAGTCAATG 377
Qy 781 TTTATGTTGAGAACTAAGGATATTTTTCAGAGAGAAATATTTTCCCTTTATCCCCAC 840
Db |||||
376 TTTATGTTGAGAACTAAGGATATTTTTCAGAGAGAAATATTTTCCCTTTATCCCCAC 317
Qy 841 TGTGTCGAGGTTTCTGTACTGCTGGATGCTGTAAGATCCCGGAGCCTTGGCGC 900
Db |||||
316 TGTGTCGAGGTTTCTGTACTGCTGGATGCTGTAAGATCCCGGAGCCTTGGCGC 257
Qy 901 ACTGCGCTTGGGTTGGCTTGGCGCTC 926
Db |||||
256 ACTGCGCTTGGGTTGGCTTGGCGCTC 231
RESULT 6
AAS34995/C
ID AAS34995 standard; cDNA; 1187 BP.
XX
AC AAS34995;
XX
DT 04-DEC-2001 (first entry)
XX

DE	cDNA encoding novel human neoplastic disease associated polypeptide #229.	
XX	Human; neoplastic disease associated polypeptide; cancer; gene therapy;	PR 14-SEP-2000; 2000US-0233063BP
KW	hyperproliferative disorder; neural disorder; immune system disorder;	PR 14-SEP-2000; 2000US-0233064P
KW	muscular disorder; reproductive disorder; Gastrointestinal disorder;	PR 14-SEP-2000; 2000US-0233065P
KW	pulmonary disorder; cardiovascular disorder; renal disorder;	PR 21-SEP-2000; 2000US-0234223P
KW	neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.	PR 21-SEP-2000; 2000US-0234274P
XX		PR 25-SEP-2000; 2000US-0234997P
OS		PR 25-SEP-2000; 2000US-0234998P
XX		PR 26-SEP-2000; 2000US-023484P
XX		PR 27-SEP-2000; 2000US-0235836P
PN		PR 27-SEP-2000; 2000US-0235836P
XX		PR 29-SEP-2000; 2000US-0236327P
PD		PR 29-SEP-2000; 2000US-0236367P
XX		PR 29-SEP-2000; 2000US-0236368P
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XX		PR 08-DEC-2000; 2000US-0251856P

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PR	19-MAY-2000;	2000US-0205515P.
PR	07-JUN-2000;	2000US-0209467P.
PR	28-JUN-2000;	2000US-0214886P.
PR	30-JUN-2000;	2000US-0215135P.
PR	07-JUL-2000;	2000US-0216647P.
PR	07-JUL-2000;	2000US-0216880P.
PR	11-JUL-2000;	2000US-0217487P.
PR	11-JUL-2000;	2000US-0217496P.
PR	14-JUL-2000;	2000US-0218290P.
PR	26-JUL-2000;	2000US-0220963P.
PR	26-JUL-2000;	2000US-0220964P.
PR	14-AUG-2000;	2000US-0224518P.
PR	14-AUG-2000;	2000US-0224519P.
PR	14-AUG-2000;	2000US-0225213P.
PR	14-AUG-2000;	2000US-0225214P.
PR	14-AUG-2000;	2000US-0225266P.
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PR	14-AUG-2000;	2000US-0225447P.
PR	14-AUG-2000;	2000US-0225757P.
PR	14-AUG-2000;	2000US-0225758P.
PR	14-AUG-2000;	2000US-0225759P.
PR	18-AUG-2000;	2000US-0226279P.
PR	22-AUG-2000;	2000US-0226681P.
PR	22-AUG-2000;	2000US-0226868P.
PR	22-AUG-2000;	2000US-0227182P.
PR	23-AUG-2000;	2000US-0227009P.
PR	30-AUG-2000;	2000US-0228924P.
PR	01-SEP-2000;	2000US-0229287P.
PR	01-SEP-2000;	2000US-0229343P.
PR	01-SEP-2000;	2000US-0229344P.
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PR	05-SEP-2000;	2000US-0229509P.
PR	05-SEP-2000;	2000US-0229513P.
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PR	08-SEP-2000;	2000US-0231242P.
PR	08-SEP-2000;	2000US-0231243P.
PR	08-SEP-2000;	2000US-0231244P.
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PR	08-SEP-2000;	2000US-0231414P.
PR	08-SEP-2000;	2000US-0232080P.
PR	08-SEP-2000;	2000US-0232081P.
PR	12-SEP-2000;	2000US-0231968P.
PR	14-SEP-2000;	2000US-0232397P.
PR	14-SEP-2000;	2000US-0232398P.
PR	14-SEP-2000;	2000US-0232399P.
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PR	14-SEP-2000;	2000US-0232401P.
PR	14-SEP-2000;	2000US-0233063P.
PR	14-SEP-2000;	2000US-0233064P.
PR	14-SEP-2000;	2000US-0233065P.
PR	21-SEP-2000;	2000US-0234223P.
PR	21-SEP-2000;	2000US-0234274P.
PR	25-SEP-2000;	2000US-0234997P.
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PR	26-SEP-2000;	2000US-0235484P.
PR	27-SEP-2000;	2000US-0235834P.
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PR	29-SEP-2000;	2000US-0236327P.
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PR	29-SEP-2000;	2000US-0236370P.
PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	13-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239935P.
PR	13-OCT-2000;	2000US-0239937P.
PR	20-OCT-2000;	2000US-0240960P.
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PR	20-OCT-2000;	2000US-0241785P.
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PR	20-OCT-2000;	2000US-0241808P.
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PR	20-OCT-2000;	2000US-0241826P.
PR	01-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
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PR	08-NOV-2000;	2000US-0246524P.
PR	08-NOV-2000;	2000US-0246525P.
PR	08-NOV-2000;	2000US-0246526P.
PR	08-NOV-2000;	2000US-0246527P.
PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
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PR	08-NOV-2000;	2000US-0246610P.
PR	08-NOV-2000;	2000US-0246611P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
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PR	17-NOV-2000;	2000US-0249212P.
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PR	17-NOV-2000;	2000US-0249216P.
PR	17-NOV-2000;	2000US-0249217P.
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PR	17-NOV-2000;	2000US-0249297P.
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PR	05-DEC-2000;	2000US-0251030P.
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PR	08-DEC-2000;	2000US-0251856P.
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PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
PR	17-JAN-2001;	2001US-00764854.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM, Barash SC;	
XX		
XX	WPI; 2003-786918/74.	
DR	P-PSDB; ADC46437.	
XX		
PT	New isolated human neoplastic disease-associated polypeptides and	
PT	polynucleotides, useful for diagnosing, preventing, prognosticating or	
PT	treating medical conditions such as cancer, AIDS, diabetes or Parkinson's	
PT	disease.	
XX		
PS	Claim 1; SEQ ID NO 239; 302pp; English.	
XX		

	CC	The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variants or species homologues). Also included are there encoding nucleic acids, a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing CC treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, CC identifying a binding partner to the polypeptide, identifying an activity in a biological assay, and the gene corresponding to the cDNA sequence.
	CC	The polypeptides, polynucleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as hyperproliferative diseases or cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematologic disorders (e.g. anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
		Query Match Best Local Similarity 99.8%; Score 924; DB 10; Length 1187; Matches 924; Conservative 1; Mismatches 1; Indels 0; Gaps 0
Qy	1	CCCCCGCCTCTCTCTCTGTAAATGCCATGCGCCCTGCAGCACACGGCCGGGC 60
Db	1156	CCCCCGCCTCTCTCTCTGTAAATGCCATGTCGCTGCAGCACACGGCCGGGC 109
Qy	61	GCTAGCGTTTCCGCTTCAGCCACCATTGGGAATGGATGAACAAGATCTGCCGCCCTGT 120
Db	1096	GCTAGCGTTTCCGCTTCAGCCACCATTGGGAATGGGATGAACAAGATCTGCCGCCCTGT 103
Qy	121	ACATCGGCAACTTCAAAGATGCCAGAGACGGGAAACAATTGAGCAAGAACAAGTGACAC 180
Db	1036	ACATCGGCAACTTCAAGATGCCAGAGACGGGAAACAATTGAGCAAGAACAAGTGACAC 977
Qy	181	ATAATTCTGTCTCCACGATAGTCCAGGCCCTATGTTGGAGGAGTTAAATACCTGTGCA 240
Db	976	ATAATTCTGTCTCCACGATAGTCCAGGCCCTATGTTGGAGGAGTTAAATACCTGTGCA 917
Qy	241	TCCCAGCAGCGGATTCACCATCTCAAAACCTGACAAAGACATTTCAAAGAAAGTATTAAT 300
Db	916	TCCCAGCAGCGGATTCACCATCTCAAAAACCTGACAAAGACATTTCAAAGAAAGTATTAAT 857
Qy	301	TCATTCACGAGTGC CGGCTCCGCGTGTAGAGCTGCCTTGTATCACTCTGGCCGGGCTCT 360
Db	856	TCATTCACGAGTGC CGGCTCCGCGTGTAGAGCTGCCTTGTATCACTCTGGCCGGGCTCT 797
Qy	361	CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db	796	CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 737
Qy	421	ATGCCCTTGCA CACCGTGGCTGTGGAGATCCTGTGCGAAACCCCAAACGTGGGCTTCCAGA 480
Db	736	ATGCCCTTGCA CACCGTGGCTGTGGAGATCCTGTGCGAAACCCCAAACGTGGGCTTCCAGA 677
Qy	481	GACAGCTCCAGAGTTTTGAGAAGCATAGAGTCCATCAGTATCGGCAGTGGCTGAGAGGAAG 540
Db	676	GACAGCTCCAGAGTTTTGAGAAGCATAGAGTCCATCAGTATCGGCAGTGGCTGAGAGGAAG 617
Qy	541	AATATGGAGAGAGCCCTTTGCAGGATGCAGAAGAGCCAAAAAATTTCTGGCCGCTCCAG 600
Db	616	AATATGGAGAGAGCCCTTTGCAGGATGCAGAAGAGCCAAAAAATTTCTGGCCGCTCCRG 557
Qy	601	GAATTCGAAAGTTC TGGGCCCTTTCTCAGAAGACTGTAATGTACCTGGAAGATTTCTGAAATA 660
Db	556	GAATTCGAAAGTTC TGGGCCCTTTCTCAGAAGACTGTAATGTACCTGGAAGATTTCTGAAATA 497
Qy	661	TTGCAAAACCCGACAGTTTTAGCTGGTCTGCCAAAAAGAAAGCAACATAGAGTTTTAAG 720
Db	496	TTGCAAAACCCGACAGTTTTAGCTGGTCTGCCAAAAAGAAAGCAACATAGAGTTTTAAG 437
Qy	721	TATCCAGTAGTGATTTGTGTAACCTTGTTTTTTCAATTTGGAAGCTGAATATATACCTAGTCATG 780


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XX SQ Sequence 1187 BP; 306 A; 290 C; 301 G; 288 T; 0 U; 2 Other;
Query Match 99.7%; Score 923.6; DB 6; Length 1187;
Best Local Similarity 99.7%; Pred. No. 6.5e-263;
Matches 923; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCCCTCCTCTCCTCCTCTGTAACATGCGCCTGCGCTGCGACACACACGCGCGGGC 60
DB 32 CCCCCTCCTCCTCCTCCTCTGTAACATGCGCCTGCGCTGCGACACACACGCGCGGGC 91
QY 61 GCTAGCGTTCGCTTCAGCACCATGCGGATGGAATGAACAAAGATCTCTGCGCGCTGT 120
DB 92 GCTAGCGTTCGCTTCAGCACCATGCGGATGGAATGAACAAAGATCTCTGCGCGCTGT 151
QY 121 ACATCGCAACTTCAAAAGATGCGAGACGCGGAAATTCAGCAAGAACAGGTGACAC 180
DB 152 ACATCGCAACTTCAAAAGATGCGAGACGCGGAAATTCAGCAAGAACAGGTGACAC 211
QY 181 ATATTCTGTCTCTCCACGATAGTGCAGCGCTTATCTTGGAGGAGTTAAATACCTGTGCA 240
DB 212 ATATTCTGTCTCTCCACGATAGTGCAGCGCTTATCTTGGAGGAGTTAAATACCTGTGCA 271
QY 241 TCCAGACGCGGATTCACATCTCAAACCTGAAGAATTCATCAAGAAATTAATAAT 300
DB 272 TCCAGACGCGGATTCACATCTCAAACCTGAAGAATTCATCAAGAAATTAATAAT 331
QY 301 TCATTTCAGAGTTCGCGCTCCGCGTGAGAGCTGCTTGTACACCTGCGCGCGGTCT 360
DB 332 TCATTTCAGAGTTCGCGCTCCGCGTGAGAGCTGCTTGTACACCTGCGCGCGGTCT 391
QY 361 CCAGGAGCTGACACTGCTGATGCGATACATCATGACCGTCACTGACTTGGCTGGGAGG 420
DB 392 CCAGGAGCTGACACTGCTGATGCGATACATCATGACCGTCACTGACTTGGCTGGGAGG 451
QY 421 ATGCCCTGCACACCGTGTGGAGATCTGTGCGCAACCCCAACCGTGGCTTCCAGA 480
DB 452 ATGCCCTGCACACCGTGTGGAGATCTGTGCGCAACCCCAACCGTGGCTTCCAGA 511
QY 481 GACAGCTCCAGGATTCAGAGCATGAGTCCATCATGTCGCGAGTGGCTGAGGAG 540
DB 512 GACAGCTCCAGGATTCAGAGCATGAGTCCATCATGTCGCGAGTGGCTGAGGAG 571
QY 541 AATATGAGAGAGCCCTTTGAGGATGCGAAGAGCCAAACAACTTCTGCGCGCTCCAG 600
DB 572 AATATGAGAGAGCCCTTTGAGGATGCGAAGAGCCAAACAACTTCTGCGCGCTCCAG 631
QY 601 GAATTCGAAGTTCTGGGCTTTCTCAGAAGACTGTAATGTAACCTGAAGTTTCTGAATA 660
DB 632 GAATTCGAAGTTCTGGGCTTTCTCAGAAGACTGTAATGTAACCTGAAGTTTCTGAATA 691
QY 661 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAAAGAACCAATAGAGTTTAA 720
DB 692 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAAAGAACCAATAGAGTTTAA 751
QY 721 TATCCAGTAGTGAATTTGAACTCTGTTTTCATTGGAAGCTGAATATATAGTACTATG 780
DB 752 TATCCAGTAGTGAATTTGAACTCTGTTTTCATTGGAAGCTGAATATATAGTACTATG 811
QY 781 TTTATGTTGAGAACTAAGATATTTCTTAGCAAGAGAAATATTTTCCCTTATCCCCAC 840
DB 812 TTTATGTTGAGAACTAAGATATTTCTTAGCAAGAGAAATATTTTCCCTTATCCCCAC 871
QY 841 TGCTGTGAGGTTTCTGTACCTCGCTTGTATGAGTCCCTGTAAGTCCCGGAGCTTCCGC 900
DB 872 TGCTGTGAGGTTTCTGTACCTCGCTTGTATGAGTCCCTGTAAGTCCCGGAGCTTCCGC 931
QY 901 ACTGCTTGTGGGTGGCTTGGCGCTC 926
DB 932 ACTGCTTGTGGGTGGCTTGGCGCTC 957
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RESULT 9

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AAF63568
ID AAF63568 standard; cDNA; 1379 BP.
XX AC AAF63568;
XX DT 11-MAY-2001 (first entry)
XX XX Human phosphatase AA374753_h coding sequence.
XX KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;
XX KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
XX KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;
XX KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
XX KW schizophrenia; hamartoma; ss.
XX OS Homo sapiens.
XX PN WO200112819-A2.
XX PD 22-FEB-2001.
XX PF 11-AUG-2000; 2000WO-US022158.
XX PR 13-AUG-1999; 99US-0149005P.
XX PA (SUGE-) SUGEN INC.
XX PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
XX WPI; 2001-211226/21.
XX DR P-PSDB; AAB73216.
XX XX New protein phosphatase polypeptide for diagnosing and treating
XX PT phosphatase related disorders such as cancer, schizophrenia, cardiac
XX PT dysfunction and/or vascular disorders.
XX PS Claim 1; Fig 4; 138pp; English.
XX CC The present invention relates to phosphatase proteins and coding
XX CC sequences. The present sequence is one such phosphatase coding sequence.
XX CC Phosphatases are enzymes that catalyse the dephosphorylation of proteins
XX CC modified by phosphorylation of serine, threonine or tyrosine residues.
XX CC The phosphatases are useful for treating a variety of diseases: for
XX CC example cancer e.g. breast, urogenital, prostate, head, neck, lung
XX CC cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung
XX CC cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach
XX CC cancer, glioblastoma, colorectal cancer and thyroid cancer,
XX CC pathophysiological hypoxia, cardiac dysfunction and/or vascular
XX CC disorders, myopathies, congenital muscle disorders, Papillon-Lefevre
XX CC syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome,
XX CC Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and
XX CC hamartomas.
XX SQ Sequence 1379 BP; 298 A; 374 C; 386 G; 320 T; 0 U; 1 Other;
Query Match 99.7%; Score 922.8; DB 4; Length 1379;
Best Local Similarity 99.8%; Pred. No. 1.2e-262;
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCCCCTCCTCCTCCTCCTGTAACATGCGCCTGCGCTGCGACACACGCGCGGGC 60
DB 257 CCCCCTCCTCCTCCTCCTGTAACATGCGCCTGCGCTGCGACACACGCGCGGGC 316
QY 61 GCTAGCGTTCGCTTCAGCACCATGCGGATGGAATGAACAAAGTCTCTGCGCGCTGT 120
DB 317 GCTAGCGTTCGCTTCAGCACCATGCGGATGGAATGAACAAAGTCTCTGCGCGCTGT 376
QY 121 ACATCGCAACTTCAAAAGATGCGAGACGCGGAAATTCAGCAAGAACAGGTGACAC 180
DB 377 ACATCGCAACTTCAAAAGATGCGAGACGCGGAAATTCAGCAAGAACAGGTGACAC 436
QY 181 ATATTCTGTCTGCTCCACGATAGTCCAGGCTCTATGTTGGAGGAGTTAAATACCTGTGCA 240
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437	ATATTCTGTCTGCCAGATAGTCCGAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA	496
241	TCCCAGCAGCGGATTACCACTCTCAAACCTGACAAGACATTTCAAAGAAGATTAAAT	300
497	TCCCAGCAGCGGATTACCACTCTCAAACCTGACAAGACATTTCAAAGAAGATTAAAT	556
301	TCATTCAAGATGCGCGCTCGCGGTGAGAGCTGCCTTGTATACATGCTGCGCGGGTCT	360
557	TCATTCAAGATGCGCGCTCGCGGTGAGAGCTGCCTTGTATACATGCTGCGCGGGTCT	616
361	CCAGGAGCTGACACTGGTGATCGCATCATCATGACGGTCACTTGACTTTGGCTGGGAGG	420
617	CCAGGAGCTGACACTGGTGATCGCATCATCATGACGGTCACTTGACTTTGGCTGGGAGG	676
421	ATGCCCTGACACCGTGCCTGGGAGATCCTGTGCCAACCCCAACGTTGGGCTTCCAGA	480
677	ATGCCCTGACACCGTGCCTGGGAGATCCTGTGCCAACCCCAACGTTGGGCTTCCAGA	736
481	GACAGCTCCAGGAGTTTGAAGCATGAGGTCATCATGATTCGGCAGTGCGCTGAAGGAAG	540
737	GACAGCTCCAGGAGTTTGAAGCATGAGGTCATCATGATTCGGCAGTGCGCTGAAGGAAG	796
541	AATATGGAGAGGCCCTTCCAGGATCCGAGAGAGCCCAAAACATTTCTGGCGGCTCCAG	600
797	AATATGGAGAGGCCCTTCCAGGATCCGAGAGAGCCCAAAACATTTCTGGCGGCTCCGG	856
601	GAATTTCTGAAGTTCTGGGCGCTTCTCAGAAGACTGTAATGTACCTGAAGTTTCTGAAATA	660
857	GAATTTCTGAAGTTCTGGGCGCTTCTCAGAAGACTGTAATGTACCTGAAGTTTCTGAAATA	916
661	TTGCCAAACCCGACAGTTTAGGCTGGTGCTGCCAAAAGAAAACCAATAGAGTTTAAAG	720
917	TTGCCAAACCCGACAGTTTAGGCTGGTGCTGCCAAAAGAAAACCAATAGAGTTTAAAG	976
721	TATCCAGTAGTGATTGTTAAACTGTTTTTTCATTTTGAAGCTGAATATATACGTAGTCATG	780
977	TATCCAGTAGTGATTGTTAAACTGTTTTTTCATTTTGAAGCTGAATATATACGTAGTCATG	1036
781	TTTATGTTGAGAACTAAGGATATTCTTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC	840
1037	TTTATGTTGAGAACTAAGGATATTCTTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC	1096
841	TGCTGTGGAGGTTTCTGTACTCGCTTGGATGCGCTGTAAGGATCCCGGAGCCTTGC CGC	900
1097	TGCTGTGGAGGTTTCTGTACTCGCTTGGATGCGCTGTAAGGATCCCGGAGCCTTGC CGC	1156
901	ACTGCCCTTGGGGTGCGCTTGGCGCTC	926
1157	ACTGCCCTTGGGGTGCGCTTGGCGCTC	1182

RESULT 10
ACC83479

ACC83479
ID ACC83479 standard; cDNA; 1520 BP.

XX

AC ACC83479;

XX
DT 08-SEP-2003 (first entry)

DE Human mitogen-activated protein kinase phosphatase X (MKPX) cDNA.

XX Mitogen-activated protein kinase phosphatase X; MKPX; enzyme; human;
KW cancer; vaccine; gene therapy; cytostatic; chromosome 6p25.3; gene; ss.
KW
XX

XX
OS

XX	Key	Location/Qualifiers
FH	CDS	449. .1003
FT		

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FT      /*tag= a
FT      /product= "Human MKPX"

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FT /note= "the CDS is also claimed in Claim 12"

XX
PN WO2003044161-A2.

30-MAY-2003.

05-NOV-2002; 2002WO-US035312.

15-NOV-2001; 2001US-0331394P.

(TULA-) TULARIK INC.

Sin WC, Yang J;

WPI; 2003-457600/43.

P-PSDB; ABR42923.

New isolated mitogen-activated protein kinase phosphatase X gene amplicon, useful for diagnosing, preventing and treating pre-cancerous lesions or cancer in a mammal, e.g. colon, prostate or ovarian cancer.

Claim 12; Page 89; 90pp; English.

The present sequence, the coding portion of which is also claimed, encodes human mitogen-activated protein kinase phosphatase X (MKPX). MKPX is amplified and overexpressed in human cancers, including colon cancer, ovarian cancer and prostate cancer. The MKPX gene, its expressed protein products and antibodies can be used diagnostically or as targets for cancer therapy or vaccine. They are also used to identify compounds and reagents useful in cancer diagnosis, prevention and therapy, and for determining the efficacy of a therapeutic treatment regimen in a patient. A claimed method of blocking *in vivo* expression of the gene involves administering a vector encoding MKPX small interfering RNA (siRNA).

Sequence 1520 BP; 348 A; 412 C; 431 G; 329 T; 0 U; 0 Other;

very Match 99.7%; Score 922.8; DB 8; Length 1520;

1st Local Similarity	99.8%;	Pred. No. 1.3e-262;	
Matches 924;	Conservative	0;	Mismatches 2;
			Indels 0;
			Gaps 0;

1 CCCCCGCGCTCCTCTCCCTGTAACATGCCATAGTGGCGCTTGGACCCACACGGCCGGGGC 60

366 CCCCGCGCTCCTCTCCCTGTAACATGCCATAGTGGCGCTGGACCAACAGGCGCGGGC 425

61 GCTAGCGTTGCGCTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCCCGGCCTGT 120

426 GCTAGCGTTTCGCTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCGCGGCCTGT 485

121 ACATCGGCAACTTCAAAGATGCCAGAGACCGCGGAACAATTGAGCAAGAACAAGGTGACAC 180

486 ACATCGGCAACTTCAAGATGCCAGAGACCGGAAACAATTGAGCAAGAACACAGGTGACAC 545

181 ATATTCTGTCTGTCCAGTACTGCCAGGCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240

546 ATATTCGTCTGTCATGATAGTGCAGGCTATGTTGGAGGAGTTAAATACCTGTGCA 605

241 TCCCAGCAGCGGATTCCACCATCTCAAAACCTGACAAGACATTTCAAAGAAAGTATTAAAT 300

606 TCCGAGCGGGATTACCATCTCAAACCTGACAACACATTTCAAAGAAAGTATTAAAT 665

301 TCATTACAGAGTGGCGGCTCCGGGTGAGAGCTGCCTTGTACACTGCCTGGCGGGGCTC 360

666 TCATTACAGATGCGGGCTCCGGGTGAGCTGCTTGTACATGCGCTGGCGGGGTCT 725

361 CCAGGAGCGTGACACTGGTGATCGCATACATGACCGTCACTGACTTTGGCTGGGAGG 420

726 CCAGGAGGTGACACTGGTGATGCCATATCATGACCGTCACTGACTTTGCTGGGAGG 785

421 ATGCCCTGCACACCCGTGGTGTGGGAGATCCTGTGCAACCCCAACGTGGGCTTCCAGA 480

786 ATGCCCTGCACACCGTGGGTGTGGGAGATCCTGTGCCAACCCCAACGTTGGCTTCCAGA 845

481 GACAGCTCCAGGAGTTTGAGAGCATGAGTCCATCAGTATCGCAGTGGCTGAAGGAAG 540

846 GACAGCTCCAGGAGTTTGAGAAGCATGAGTCCATCAGTATCGCAGTGCGTGAAGGAG 905

Db 906 AATATGGAGAGCCCTTTGAGGATGACAGAGGACCAAAACATTTGCGCGCTCCAG 965
Qy 601 GAAATTCGAAGTTCTGGCCCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAATA 660
Db 966 GAAATTCGAAGTTCTGGCCCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAATA 1025
Qy 661 TTGCAAAACCCAGAGTTTAGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 720
Db 1026 TTGCAAAACCCAGAGTTTAGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 1085
Qy 721 TATCCAGTAGTGAATTTGTAACCTTTCTTTTATTTGAAGCTGAATATATAGCTAGTCATG 780
Db 1086 TATCCAGTAGTGAATTTGTAACCTTTCTTTTATTTGAAGCTGAATATATAGCTAGTCATG 1145
Qy 781 TTTATGTTGAGAACTAAGGATATTTTATAGCAAGAGAAAATATTTTCCCTTATCCCCAC 840
Db 1146 TTTATGTTGAGAACTAAGGATATTTTATAGCAAGAGAAAATATTTTCCCTTATCCCCAC 1205
Qy 841 TGCTGTGAGGTTTCTGTACCTCGCTTGGATGCGCTGAAGGATCCCGGAGCCTTGGCGC 900
Db 1206 TGCTGTGAGGTTTCTGTACCTCGCTTGGATGCGCTGAAGGATCCCGGAGCCTTGGCGC 1265
Qy 901 ACTGCTTGTGGGTGGCTTGGCGCTC 926
Db 1266 ACTGCTTGTGGGTGGCTTGGCGCTC 1291

RESULT 12
ID ADP25000 standard; cDNA; 1520 BP.
XX ADP25000;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide encoding cDNA SEQ ID NO:2178.
XX
KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
OS Unidentified.
XX
FN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
XX
DR P-PSDB; ADP25001.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 1; SEQ ID NO 2178; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
SQ Sequence 1520 BP; 348 A; 412 C; 431 G; 329 T; 0 U; 0 Other;

Query Match 99.7%; Score 922.8; DB 13; Length 1520;
Best Local Similarity 99.8%; Pred. No. 1.3e-262;
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTGGCGCTGGACACACGCGCGGGC 60
Db 366 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTGGCGCTGGACACACGCGCGGGC 425
Qy 61 GCTAGCGTTCCGCTTCCAGCCACCATGGGAAATGGGATGAACAAGATCCTGCGCGGCTGT 120
Db 426 GCTAGCGTTCCGCTTCCAGCCACCATGGGAAATGGGATGAACAAGATCCTGCGCGGCTGT 485
Qy 121 ACATCGGCAACTTCAAGATGCCAGACGCGGAAACAATTTGAGCAAGAAAGTGAAC 180
Db 486 ACATCGGCAACTTCAAGATGCCAGACGCGGAAACAATTTGAGCAAGAAAGTGAAC 545
Qy 181 ATATTCTGTCTGTCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
Db 546 ATATTCTGTCTGTCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 605
Qy 241 TCCAGCAGCGGATTTACCATCTCAAAACCTGACAGACATTTCAAAGAAGTATTAAT 300
Db 606 TCCAGCAGCGGATTTACCATCTCAAAACCTGACAGACATTTCAAAGAAGTATTAAT 665
Qy 301 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGCTGCCCTGTACACTGCTGCGCGGGTCT 360
Db 666 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGCTGCCCTGTACACTGCTGCGCGGGTCT 725
Qy 361 CCAGGAGCGTGACACTGGTGATGCGATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 726 CCAGGAGCGTGACACTGGTGATGCGATACATCATGACCGTCACTGACTTTGGCTGGGAGG 785
Qy 421 ATGCCCTGCAACCGTGGCTGCTGGGAGATCTGTGCAACCCCAACCGTGGGCTTCCAGA 480
Db 786 ATGCCCTGCAACCGTGGCTGCTGGGAGATCTGTGCAACCCCAACCGTGGGCTTCCAGA 845
Qy 481 GACAGCTCCAGGAGTTTGAAGCATGAGTCCATCAGTATCGGACGTGGCTGAAGGAAG 540
Db 846 GACAGCTCCAGGAGTTTGAAGCATGAGTCCATCAGTATCGGACGTGGCTGAAGGAAG 905
Qy 541 AATATGAGAGAGCCCTTTGCGAGGATGCAGAAAGCCAAAACATTTCTGGCCGCTCCAG 600
Db 906 AATATGAGAGAGCCCTTTGCGAGGATGCAGAAAGCCAAAACATTTCTGGCCGCTCCAG 965
Qy 601 GAATTCGAAGTTCTGGCCCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAATA 660
Db 966 GAATTCGAAGTTCTGGCCCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAATA 1025
Qy 661 TTGCAAAACCCAGAGTTTAGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 720

Db 1026 TTGCAACCCACAGAGTTTAGCTGCTGTCACAAAAGAAAGCAACATAGAGTTTAAG 1085
 Qy 721 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 780
 Db 1086 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 1145
 Qy 781 TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 840
 Db 1146 TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 1205
 Qy 841 TGCTGTGAGGTTTCTGACCTCGCTTGATGCGCTGTAAGATCCCGGAGCCTTGCCGC 900
 Db 1206 TGCTGTGAGGTTTCTGACCTCGCTTGATGCGCTGTAAGATCCCGGAGCCTTGCCGC 1265
 Qy 901 ACTGCTTGTGGTGGCTTTGGCGCTC 926
 Db 1266 ACTGCTTGTGGTGGCTTTGGCGCTC 1291

RESULT 13
 AAZ46164
 ID AAZ46164 standard; cDNA; 1290 BP.
 AC AAZ46164;
 XX
 DT 16-MAY-2000 (first entry)
 XX

DE cDNA sequence encoding a human phosphorylation effector PHSP-27.

XX Human; phosphorylation effector; PHSP; proliferative disorder;
 KW immune disorder; neuronal disorder; ss.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 238..792
 CDS /*tag= a
 FT /*product= "phosphorylation effector"
 XX

FN WO200006728-A2.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017132.

XX 28-JUL-1998; 98US-0155213P.

PR 14-SEP-1998; 98US-0155196P.

PR 14-OCT-1998; 98US-0155239P.

PR 03-NOV-1998; 98US-0106889P.

PR 19-NOV-1998; 98US-0109093P.

PR 22-DEC-1998; 98US-0113796P.

PR 12-JAN-1999; 99US-0155233P.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;

PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;

PI Reddy R, Lu DAM, Shih LL;

XX WPI; 2000-183125/16.

DR P-PSDB; AAY68795.

XX New human phosphorylation effectors useful for the diagnosis, treatment

PT and prevention of proliferative, immune and neuronal disorders.

XX Claim 9; Page 139; 142pp; English.

XX AAZ46138-246168 encode human phosphorylation effectors (PHSP), designated

CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the

CC specification). The sequences were isolated from cDNA libraries prepared

CC from various human tissues. The PHSP proteins are useful for the

CC diagnosis, treatment and prevention of proliferative disorders, immune

CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical
 CC compositions which useful for treating or preventing disorders associated
 CC with decreased PHSP expression/activity. PHSP antagonists are useful for
 CC treating or preventing disorders associated with increased PHSP
 CC expression/activity
 XX

SQ Sequence 1290 BP; 299 A; 341 C; 339 G; 311 T; 0 U; 0 Other;

Query Match 99.5%; Score 921.2; DB 3; Length 1290;

Best Local Similarity 99.7%; Pred. No. 3.5e-262;

Matches 923; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTGCCTGCGACACACGCGCGGCG 60

Db 155 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTGCCTGCGACACACGCGCGGCG 214

Qy 61 GCTAGCGTTGCGCTTCAGCCACCATGGGAATGGGATGGAACAAGATCCTGCCGCGCTGT 120

Db 215 GCTAGCGTTGCGCTTCAGCCACCATGGGAATGGGATGGAACAAGATCCTGCCGCGCTGT 274

Qy 121 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGAAACAATTCAGCAAGAAACAAGGTGACAC 180

Db 275 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGAAACAATTCAGCAAGAAACAAGGTGACAC 334

Qy 181 ATATTCTGTCTGCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240

Db 335 ATATTCTGTCTGCCACGATAGTCCAGGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA 394

Qy 241 TCCAGAGCGGATTCACATCTCAAAACCTGACAGACATTTCAAGAAAGATTAAT 300

Db 395 TCCAGAGCGGATTCACATCTCAAAACCTGACAGACATTTCAAGAAAGATTAAT 454

Qy 301 TCATTACAGAGTCCGCGCTCGCGGTGAGAGTCCCTTGACACCTGCTGCGCGGGTCT 360

Db 455 TCATTACAGAGTCCGCGCTCGCGGTGAGAGTCCCTTGACACCTGCTGCGCGGGTCT 514

Qy 361 CCAGGAGCTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420

Db 515 CCAGGAGCTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 574

Qy 421 ATGCCCTGCACACCGTGGTGCTGGGAGATCCTGTGCCAACCCCAACCTGGGCTTCCAGA 480

Db 575 ATGCCCTGCACACCGTGGTGCTGGGAGATCCTGTGCCAACCCCAACCTGGGCTTCCAGA 634

Qy 481 GACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGTATCGGCAGTGGCTGAAGGAAG 540

Db 635 GACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGTATCGGCAGTGGCTGAAGGAAG 694

Qy 541 AATATGAGAGAGAGCCCTTTGAGGATGCAAGAAAGCCCAAAACATTTCTGCCCGCTCCAG 600

Db 695 AATATGAGAGAGAGCCCTTTGAGGATGCAAGAAAGCCCAAAACATTTCTGCCCGCTCCAG 754

Qy 601 GAATTCCTGAAGTTCTGGGCTTTCTCAGAGACTGTAAATGTACCTGAAGTTTCTGAATA 660

Db 755 GAATTCCTGAAGTTCTGGGCTTTCTCAGAGACTGTAAATGTACCTGAAGTTTCTGAATA 814

Qy 661 TTGCAAAACCCAGAGTTTAGGCTGGTGGTCCCAAAAGAAAGCAACATAGTTTAAG 720

Db 815 TTGCAAAACCCAGAGTTTAGGCTGGTGGTCCCAAAAGAAAGCAACATAGTTTAAG 874

Qy 721 TATCCAGTAGTGAATTTGTAAACTTTTTCATTTGAAGCTGAATATATAGTGTATG 780

Db 875 TATCCAGTAGTGAATTTGTAAACTTTTTCATTTGAAGCTGAATATATAGTGTATG 934

Qy 781 TTTATGTTGAGAACTAAGGATATTTTAGCAAGAGAAATATTTTCCCTTATCCCCAC 840

Db 935 TTTATGTTGAGAACTAAGGATATTTTAGCAAGAGAAATATTTTCCCTTATCCCCAC 994

Qy 841 TGCTGTGAGGTTTCTGACCTCGCTGGATGCGCTGTAAGGATCCCGGAGCCTTGCGGC 900

Db 995 TGCTGTGAGGTTTCTGACCTCGCTGGATGCGCTGTAAGGATCCCGGAGCCTTGCGGC 1054

Qy 901 ACTGCTTGTGGTGGCTTTGGCGCTC 926

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1055 ACTGCTTGTGGTGGCTTGGCGCTC 1080

RESULT 14
ABV28356
ID ABV28356 standard; cDNA; 1161 BP.
XX AC
XX ABV28356;
XX DT
XX 16-SEP-2002 (first entry)
XX DE
XX Human prostate expression marker cDNA 28347.
XX KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW
XX pharmacogenomic marker; gene; ss.
XX OS
XX Homo sapiens.
XX XX
XX WO200160860-A2.
XX PD
XX 23-AUG-2001.
XX PF
XX 20-FEB-2001; 2001WO-US005171.
XX PP
XX 20-FEB-2001; 2001WO-US005171.
XX PR
XX 17-FEB-2000; 2000US-0183319P.
XX PR
XX 16-MAR-2000; 2000US-0189862P.
XX PR
XX 25-MAY-2000; 2000US-0207454P.
XX PR
XX 09-JUN-2000; 2000US-0211314P.
XX PR
XX 18-JUL-2000; 2000US-0219007P.
XX PR
XX 13-DEC-2000; 2000US-0255281P.
XX PR
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA
XX Schlegel R, Endege WO, Monahan JE;
XX PI
XX WPI; 2001-662795/76.
XX DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX XX
XX Claim 1; Page 5908-5909; 11750pp; English.
XX PS
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX CC
XX SQ
XX Sequence 1161 BP; 301 A; 274 C; 299 G; 278 T; 0 U; 9 Other;

Query Match          96.6%; Score 894.2; DB 5; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-254;
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 GCCATAGTGCCTGCGACACACACGGCGGGCGCTAGCGTTGCGCTTCAGCCACCATGG 87
DB 7 GGCCTAGTGGCTCGGACCAACACGGCGGGCGCTAGCGTTGCGCTTCAGCCACCATGG 66
QY 88 GGAATGGGATGAAACAGATCTGCCCGGCTGTACATCGGCAACTTCAAAGATGCCAGAG 147
DB 67 GGAATGGGATGAAACAGATCTGCCCGGCTGTACATCGGCAACTTCAAAGATGCCAGAG 126
QY 148 ACGCGGAACAATTGAGCAAGAACAGGTGACACATATTCTGTCTGCCACGATAGTGCCA 207
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DB 127 ACGCGGAACAATTGAGCAAGAACAGGTGACACATATTCTGTCTGTCCACGATAGTGCCA 186
QY 208 GGCTATGTTGGAGGGAGTTAAATACCTGTGCAATCCAGCAGCGGATTCACCATCTCAAA 267
DB 187 GGCTATGTTGGAGGGAGTTAAATACCTGTGCAATCCAGCAGCGGATTCACCATCTCAAA 246
QY 268 ACCTGACACACATTTCAAAGAAAGTATTAAATTCATTTCAGAGTCCGGCTCCGGCGTG 327
DB 247 ACCTGACACACATTTCAAAGAAAGTATTAAATTCATTTCAGAGTCCGGCTCCGGCGTG 306
QY 328 AGAGTCCCTTGTACACTGCTGCCCGGGTCTCCAGGAGCGTGACACTGGTATCGCAT 387
DB 307 AGAGTCCCTTGTACACTGCTGCCCGGGTCTCCAGGAGCGTGACACTGGTATCGCAT 366
QY 388 ACATCATGACCGTCACTGACTTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGGGA 447
DB 367 ACATCATGACCGTCACTGACTTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGGGA 426
QY 448 GATCCTGTGCAACCCCAACGTCGGCTTCCAGAGACAGCTCCAGGAGTTTGAGNAGCATG 507
DB 427 GATCCTGTGCAACCCCAACGTCGGCTTCCAGAGACAGCTCCAGGAGTTTGAGNAGCATG 486
QY 508 AGGTCCATCAGTATCGGCACTGCTGAAGGAAGTATGAGAGAGCGCTTTTGAGGATG 567
DB 487 AGGTCCATCAGTATCGGCACTGCTGAAGGAAGTATGAGAGAGCGCTTTTGAGGATG 546
QY 568 CAGAAGAAAGCAAAACATTTCTGCCGCTCCAGGAAATTTGAAAGTTCTGGGCTTTCTCA 627
DB 547 CAGAAGAAAGCAAAACATTTCTGCCGCTCCAGGAAATTTCTGAAAGTTCTGGGCTTTCTCA 606
QY 628 GAAGACTGTAATGTACCTGAAGTTTCTGAATATTTGCAATATTTGCAATATTTGAGGCTGGT 687
DB 607 GAAGACTGTAATGTACCTGAAGTTTCTGAATATTTGCAATATTTGCAATATTTGAGGCTGGT 666
QY 688 GCTGCCAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGAATTTGTAATCTGTT 747
DB 667 GCTGCCAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGAATTTGTAATCTGTT 726
QY 748 TTTCATTTGAAGCTGAATATATACGTAGTCAATGTTTAAAGTATGAGAACTAAGGATATCTT 807
DB 727 TTTCATTTGAAGCTGAATATATACGTAGTCAATGTTTAAAGTATGAGAACTAAGGATATCTT 786
QY 808 TAGCAGAGAAATATTTTCCCTTATCCCACTGCTGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 867
DB 787 TAGCAGAGAAATATTTTCCCTTATCCCACTGCTGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 846
QY 868 GGATGCTGTAAGGATCCCGGAGCCTTGGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 926
DB 847 GGATGCTGTAAGGATCCCGGAGCCTTGGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 905

RESULT 15
ABV22541
ID ABV22541 standard; cDNA; 1161 BP.
XX AC
XX ABV22541;
XX DT
XX 13-SEP-2002 (first entry)
XX DE
XX Human prostate expression marker cDNA 22532.
XX KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW
XX pharmacogenomic marker; gene; ss.
XX OS
XX Homo sapiens.
XX XX
XX WO200160860-A2.
XX PD
XX 23-AUG-2001.
XX PF
XX 20-FEB-2001; 2001WO-US005171.
XX PP
XX 17-FEB-2000; 2000US-0183319P.
XX PR
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PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 3939; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 1161 BP; 301 A; 274 C; 299 G; 278 T; 0 U; 9 Other;

Query Match 96.6%; Score 894.2; DB 5; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-25;
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 GCCATAGTGCCTGCGACACACGCGCGGGCGCTAGCGTTGCGCTTCAGCCACCATGG 87
DB 7 GGCCTAGTGCCTGCGACACACGCGCGGGCGCTAGCGTTGCGCTTCAGCCACCATGG 66

QY 88 GGAATGGGATGAACAAGATCTGCGCGGGCGCTGTACATCGGCAACTTCAAAGATGCCAG 147
DB 67 GGAATGGGATGAACAAGATCTGCGCGGGCGCTGTACATCGGCAACTTCAAAGATGCCAG 126

QY 148 ACGGGACAAATTGACGAAGACAGGTGACACATATCTGCTGTCCACGATAGTGCCA 207
DB 127 ACGGGACAAATTGACGAAGACAGGTGACACATATCTGCTGTCCACGATAGTGCCA 186

QY 208 GGCCTATGTTGGAGGAGTAAATACCTGTGCATCCGACGCGGATTCACCATCTCAA 267
DB 187 GGCCTATGTTGGAGGAGTAAATACCTGTGCATCCGACGCGGATTCACCATCTCAA 246

QY 268 ACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTACAGAGTCCGGCTCCCGGGTG 327
DB 247 ACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTACAGAGTCCGGCTCCCGGGTG 306

QY 328 AGAGTGCCTGTACATGCTGCGCGGGGTCTCCAGGAGCGTGACACTGCTGATCGCAT 387
DB 307 AGAGTGCCTGTACATGCTGCGCGGGGTCTCCAGGAGCGTGACACTGCTGATCGCAT 366

QY 388 ACATCATGACCGTCACTGACTTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGGGA 447
DB 367 ACATCATGACCGTCACTGACTTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGGGA 426

QY 448 GATCTGTGCCAAACCCCAACGTTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATG 507
DB 427 GATCTGTGCCAAACCCCAACGTTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATG 486

QY 508 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCAGGATG 567
DB 487 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCAGGATG 546

QY 568 CAGAAGAAGCCAAACAAATTTCTGCCCGCTCCAGGAATTTCTGAAGTTCTGGCGCTTTCTCA 627
DB 547 CAGAAGAAGCCAAACAAATTTCTGCCCGCTCCAGGAATTTCTGAAGTTCTGGCGCTTTCTCA 606

QY 628 GAAGACTGTAAATGTACCTGAAGTTTCTGAATATTTGCAACCCCGCAGAGTTTAGGCTGGT 687
DB 607 GAAGACTGTAAATGTACCTGAAGTTTCTGAATATTTGCAACCCCGCAGAGTTTAGGCTGGT 666

QY 688 GCTGCCAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGATTTGTAAACTTCTT 747
DB 667 GCTGCCAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGATTTGTAAACTTCTT 726

QY 748 TTTCAATTTGAAGCTGAATATATACGTAGTCAATGTTTATGTTGAGAACTAAGGATATCTT 807
DB 727 TTTCAATTTGAAGCTGAATATATACGTAGTCAATGTTTATGTTGAGAACTAAGGATATCTT 786

QY 808 TAGCAAGAGAAATATTTTCCCTTATCCCGCTGCTGTGAGAGTTTCTGTACCTCGCTT 867
DB 787 TAGCAAGAGAAATATTTTCCCTTATCCCGCTGCTGTGAGAGTTTCTGTACCTCGCTT 846

QY 868 GGATGCTGTAAAGGATCCCGGAGGCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 926
DB 847 GGATGCTGTAAAGGATCCCGGAGGCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 905

Search completed: July 21, 2005, 13:31:59
Job time : 619 secs

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OM protein - protein search, using sw model

Run on: July 21, 2005, 17:59:27 ; Search time 334 Seconds
(without alignments)

282.104 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNGMKILPGLYIGNFKDA.....AKNIIAAPGLKFWAFLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	184	2 Q9NRW4	Q9nrw4 homo sapien
2	932	95.6	184	2 Q9NRW4	Q9nrw4 mus musculus
3	715	73.3	209	2 Q6GQJ8	Q6gqj8 xenopus lae
4	557	57.1	208	2 Q6GQJ8	Q6gqj8 xenopus lae
5	544	55.8	209	2 Q6GQJ8	Q6gqj8 xenopus lae
6	528	54.2	235	2 Q6PGN7	Q6pgn7 mus musculus
7	482	49.4	327	2 Q8IQK1	Q8iqk1 drosophila
8	482	49.4	327	2 Q8IQK1	Q8iqk1 drosophila
9	453	46.5	327	2 Q8IQK0	Q8iqk0 drosophila
10	444	45.5	295	1 DUSF_HUMAN	DUSF_HUMAN
11	438	44.9	81	2 Q6GAR1	Q6gar1 mus musculus
12	428	43.9	191	2 Q7PV27	Q7pv27 anopheles g
13	420	43.1	125	1 DUSF_MOUSE	DUSF_MOUSE
14	297	30.5	201	2 Q86F24	Q86f24 schistosoma
15	259	26.6	476	2 Q86JT3	Q86jt3 dictyosteli
16	257.5	26.4	542	2 Q7PV94	Q7pv94 anopheles g
17	250.5	25.7	483	1 DUSA_MOUSE	DUSA_MOUSE
18	249.5	25.6	384	2 Q6P9C2	Q6p9c2 mus musculus
19	247.5	25.4	383	2 Q8UW48	Q8uw48 figu rubrip
20	247	25.3	707	2 Q7QTA9	Q7qta9 giardia lam
21	246.5	25.3	177	2 Q8CSL5	Q8csl5 mus musculus
22	246.5	25.3	362	2 Q803B2	Q803b2 brachydanio
23	246.5	25.3	364	2 Q6NYH0	Q6nyh0 brachydanio
24	246.5	25.3	482	1 DUSA_HUMAN	DUSA_HUMAN
25	246.5	25.3	483	2 Q8R3L3	Q8r3l3 m dusp10 pr
26	245.5	25.2	269	2 Q7POA9	Q7poa9 anopheles g
27	245.5	25.2	354	2 Q8N4A4	Q8n4a4 homo sapien
28	245.5	25.2	378	1 DUS9_HUMAN	DUS9_HUMAN
29	244.5	25.1	384	1 DUS6_MOUSE	DUS6_MOUSE
30	244.5	25.1	381	1 DUS6_MOUSE	DUS6_MOUSE
31	244.5	25.1	381	1 DUS6_MOUSE	DUS6_MOUSE

32	244.5	25.1	381	1 DUS6_RAT	Q64346 rattus norv
33	244.5	25.1	382	2 Q7T2L9	Q7t2l9 gallus gall
34	244.5	25.1	482	2 Q6IAR2	Q6iar2 homo sapien
35	243.5	25.0	476	2 Q3VHV8	Q3vhv8 drosophila
36	243	24.9	653	2 Q7T2T3	Q7t2t3 xenopus lae
37	243	24.9	691	2 Q6IVY4	Q6ivy4 xenopus lae
38	243	24.9	694	2 Q68ET3	Q68et3 xenopus lae
39	242.5	24.9	196	2 Q8LPY0	Q8lpy0 oryza sativ
40	242.5	24.9	198	2 Q9LUG6	Q9lugu arabidopsis
41	242.5	24.9	198	2 Q9ZR37	Q9zr37 arabidopsis
42	242.5	24.9	382	2 Q7T2L8	Q7t2l8 brachydanio
43	240.5	24.7	167	2 Q8M8K7	Q8m8k7 arabidopsis
44	240	24.6	241	2 Q9VVM4	Q9vvw4 drosophila
45	240	24.6	290	2 Q86P14	Q86p14 drosophila

ALIGNMENTS

RESULT 1

ID	Q9NRW4	PRELIMINARY;	PRT;	184 AA.
AC	Q9NRW4;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	Mitogen-activated protein kinase phosphatase x (JNK-stimulating phosphatase 1) (Dual specificity phosphatase 22) (LMW-DSP2).			
GN	Name=MKPX; Synonyms=DUSP22, JSP1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,			
RA	Tu Y., Gu W., Fu G., Huang C.;			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21574601; PubMed=11717427; DOI=10.1073/pnas.231499098;			
RA	Shen Y., Luche R., Wei B., Gordon M.D., Diltz C.D., Tonks N.K.;			
RT	"Activation of the Jnk signaling pathway by a dual-specificity phosphatase, JSP-1."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:13613-13618(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.;			

```

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Cheng H.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165519; AAF6649.1; -
DR EMBL; AF424702; AAL18850.1; -
DR EMBL; BC022847; AAL22847.1; -
DR EMBL; AY249859; AAP76376.1; -
DR HSP; Q16828; 1MKP.
DR Genew; HGNC:16077; DUSP22.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0000188; P:inactivation of MAPK; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000340; DS phosphatase.
DR PROSITE; PS000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR InterPro; IPR000387; DS phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
DR Kinase.
SQ SEQUENCE 184 AA; 20910 MW; B3F962A087C2BA20 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.6e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
Db 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60

Qy 61 QNLTRHFKESIKFIEHCRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFIEHCRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKTFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKTFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 2
Q99N11 PRELIMINARY; PRT; 184 AA.
AC Q99N11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Dual specificity phosphatase TS-DSP2.
GN Name=Dusp22;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347909; PubMed=11346645; DOI=10.1074/jbc.M100408200;
RA Aoyama K., Nagata M., Oshima K., Matsuda T., Aoki N.;
RT "Molecular cloning and characterization of a novel dual specificity
RT phosphatase, LMW-DSP2, that lacks the cdc25 homology domain.";
RL J. Biol. Chem. 276:27575-27583(2001).
DR EMBL; AF237619; AAK15038.1; -
DR HSP; Q16828; 1MKP.
DR MGD; MGI:1915926; Dusp22.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0046330; P:positive regulation of JNK cascade; IDA.
DR GO; GO:0042127; P:regulation of cell proliferation; IMP.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IMP.

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DR InterPro; IPR000340; DS phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 184 AA; 20997 MW; 649553325E88AB577 CRC64;

Query Match 95.6%; Score 932; DB 2; Length 184;
Best Local Similarity 93.5%; Pred. No. 8.9e-83;
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
Db 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60

Qy 61 QNLTRHFKESIKFIEHCRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFIEHCRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKTFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGENPLRDABEAKNLAAPGILKTFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 3
Q6GQJ8 PRELIMINARY; PRT; 209 AA.
AC Q6GQJ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC79099 protein.
GN Name=MGC79099;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;

```

"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative."
Dev. Dyn. 225:384-391(2002).
[3]

RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072744; AAH72744.1; -
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. . .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE 1;
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 209 AA; 23485 MW; E83FB752048C902E CRC64;

Query Match 73.3%; Score 715; DB 2; Length 209;
Best Local Similarity 75.1%; Pred. No. 1.6e-61;
Matches 127; Conservative 21; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNGGNKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGVKYLICIPADSPS 60
DB 1 MNGGNKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGVKYLICIPADSPS 60
QY 61 QNLTREPKESIKFTHICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120
DB 61 QNLTREPKESIKFTHICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120
QY 121 GRSCANPNVGFQRLQEFKEHVEHVOYRWLKEEYGESPLQDAEAKNLL 169
DB 121 ARTCANPNMGKQLEDFGKCEVHFRTWLKDYTESFTHDKDAKQLL 169

RESULT 4
Q6DQ6 PRELIMINARY; PRT; 208 AA.
AC Q6DQ6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:92816.
GN Name=zgc:92816;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076284; AAH76284.1; -
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. . .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1;
DR PROSITE; PS0056; TYR_PHOSPHATASE 2;
DR PROSITE; PS0054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase.
SQ SEQUENCE 208 AA; 23396 MW; 5B148AE083808854 CRC64;

Query Match 57.1%; Score 557; DB 2; Length 208;
Best Local Similarity 57.6%; Pred. No. 4.2e-46;
Matches 98; Conservative 36; Mismatches 36; Indels 0; Gaps 0;

QY 1 MNGGNKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGVKYLICIPADSPS 60
DB 1 MNGGNKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGVKYLICIPADSPS 60
QY 61 QNLTREPKESIKFTHICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120
DB 61 QNLTREPKESIKFTHICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120
QY 121 GRSCANPNVGFQRLQEFKEHVEHVOYRWLKEEYGESPLQDAEAKNLL 170
DB 121 VRSFVGNVGFQRLQEFKEHVEHVOYRWLKEEYGESPLQDAEAKNLL 170

RESULT 5
Q6GQZ9 PRELIMINARY; PRT; 209 AA.
AC Q6GQZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC82394 protein.
GN Name=MGC82394;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
 Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 EMBL; AE003537; AAN11825.1; -
 EMBL; BT014928; AAT47779.1; -
 HSSP; Q16828; IMKP.
 FlyBase; FBgn0036369; CG10089.
 GO; GO:0008138; P:protein tyrosine/serine/threonine phosphatase. . . ; IEA.
 GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 InterPro; IPR000340; DS_phosphatase.
 InterPro; IPR000387; TYR_phosphatase.
 Pfam; PF00782; DSPC; 1.
 SMART; SM00195; DSPC; 1.
 PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 SQ SEQUENCE 327 AA; 36855 MW; 2DAEF208A843FAE3 CRC64;

Query Match 49.4%; Score 482; DB 2; Length 327;
 Best Local Similarity 51.8%; Pred. No. 1.5e-38;
 Matches 86; Conservative 36; Mismatches 44; Indels 0; Gaps 0

QY 1 MNGMNMKILPGLYIGNPKDARDARQLSKNVKTHILSVHDSARPMLEGVKYLCPAADSFS 60
 DB 1 MNGMNMKVLPGLYVGNVYRDSKDHQAERFKFISHIIAHTDSPRLLPDKHYLCVMASDTPD 60
 QY 61 QNLTTRHFKEISKIHECRILGESCLVHCLAGVSRSVLVIAYIMTVDFGHEDELHTVRA 120
 DB 61 QNLSSQYFVSGVNCDFIHAARLREGNVLIHCLAGMSRSVTVAIVYIMTATHLNKEALKVYRA 120
 QY 121 GRSCAMPNVGFQRLQEFKEHVEHVQWLKKEEYGESPLQDAEAK 166
 DB 121 GRAVPNAGFQSLQEFQKLEERRRURKRPSSALEQLDRTK 166

RESULT 8
 ID Q9VU80 PRELIMINARY; PRT: 447 AA.
 AC Q9VU80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG10089.PD.
 GN ORFNames=CG10089;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20136006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.J., Blasej G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abiril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Deyanov A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Drommler B., Carlson J., Svirska R.,
RA Patel S., Frise E., Wheeler K.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003537; AAN11827.1; -
DR HSSP; Q16828; 1MKP.
DR FlyBase; FBgn0036369; CG10089.
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphatase. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS phosphatase.
DR InterPro; IPR000387; TVR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE DUAL; 1.
SQ SEQUENCE 327 AA; 37007 MW; F79A75EC9CAE9BC7 CRC64;

Query Match 46.5%; Score 453; DB 2; Length 327;
Best Local Similarity 50.0%; Pred. No. 1e-35;
Matches 81; Conservative 36; Mismatches 45; Indels 0; Gaps 0;

Oy 5 MNKILPGLYIGNFKDARDAEQLSKNVKTHILSVHDSAPMLLEGVKYLCIPADSPSONLT 64
Db 5 MGKVLPLGVNGYRDKDHAQERFKISHIATIDSPRLPLDPKHYLCVWASDTPDQNL 64
Oy 65 RHFKESIKFTIECRILRGSCILVHCLAGVSRSTVIVAYIMVTDFGWEDALHTVAGRSC 124
Db 65 QYFVSCNDFIHAARLREGNVLHCLAGVSRSTVIVAYIMVTATHLNKEALKVVRAGRAV 124
Oy 125 ANPNVGFQRLQEPKEVHQVROWLKEEYGESPLQDAEAK 166
Db 125 ANPNAGFQSLQEPKEVHQVROWLKEEYGESPLQDAEAK 166

RESULT 10
ID DUSF_HUMAN STANDARD; PRT; 295 AA.
AC Q9H1R2; Q9H262; Q9BX24;
DT 28-FEB-2003 (Rel. 41, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).
GN Name=DUSP15; Synonyms=C20orf57;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yaeuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,
RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RN Nat. Genet. 36:40-45(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.M., Lawlor S.,
RA Lehar V.L., Martin S.L., Leversha M.A., Lloyd C., Lloyd D.M., Lawlor S.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).


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Db 1 MTVTDFGWEDALHTVAGRSANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAE 60
QY 164 EAKNIIAAPGILKFWAFRLRL 184
Db 61 EAKNIIAAPGILKFWAFRLRL 81

RESULT 12
Q7PV27 ID Q7PV27 PRELIMINARY; PRT; 191 AA.
AC Q7PV27;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANGP0000016462 (Fragment).
GN Name=ENSANGG0000013973;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0501008986; EAA00578.2; -.
DR HSSP; P51452; 1JAX.
DR GO; GO:0008139; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
FT NON_TER 1
FT NON_TER 191
SQ SEQUENCE 191 AA; 21875 MW; 28DA4C22B83B853D CRC64;

Query Match 43.9%; Score 428; DB 2; Length 191;
Best Local Similarity 48.8%; Pred. No. 1.5e-33;
Matches 80; Conservative 36; Mismatches 48; Indels 0; Gaps 0;

QY 7 KILPGLYGNFKDARDABQLSKNKKVTHILSVHDSARPMLGVKYLICIPAADSPQNLTNRH 66
Db 1 QVMPGLYIGNYRDSKDYQQLDRYGITHIVSIHDSPRFHPDKHYLCVIAADKPDQNLQSY 60
QY 67 FKESIKFTHECRLGESCLVHCLAGVSRVTLVIAYIMVTDFGWEDALHTVAGRSAN 126
Db 61 FSVCNDFHISARLKGQVLIHCLAGMSRVTVAIVIMCVTPLSKWEALKVVRGRSTAN 120
QY 127 PNVGQRQLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNIIA 170
Db 121 PNLGPNQLQDFETNKLTEERRRLKRPSPSLALELTDEKQCYLEA 164

RESULT 13
DUSF_MOUSE ID DUSF_MOUSE STANDARD; PRT; 125 AA.
AC Q8R4V2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (Fragment).
DE (Dual specificity protein phosphatase T-DSP10) (Fragment).
GN Name=Dusp15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RX MEDLINE=21326039; PubMed=11432789;
RA Aoki N., Aoyama K., Nagata M., Matsuda T.;
RT "A growing family of dual specificity phosphatases with low molecular
RT masses.";
RL J. Biochem. 130:133-140(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21671825; PubMed=11812828; DOI=10.1093/nar/29.24.4983;
RA Mu X., Zhao S., Pershad R., Haiech T.-F., Scarpa A., Wang S.W.,
RA White R.A., Beremand P.D., Thomas T.L., Gan L., Klein W.H.;
RT "Gene expression in the developing mouse retina by EST sequencing and
RT microarray analysis.";
RL Nucleic Acids Res. 29:4983-4993(2001).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8R4V2-1; Sequence=Displayed;
CC Note=Derived from EST data;
CC Name=2;
CC IsoId=Q8R4V2-2; Sequence=VSP_007294, VSP_007295;
CC Note=Inactive. Lacks the active site;
CC -!- TISSUE SPECIFICITY: Isoform 2 is highly expressed in testis.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class dual specificity subfamily.
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EMBL; AF357887; AAM00226.1; -
DR EMBL; BU924460; -; NOT_ANNOTATED_CDS.
DR HSSP; P51452; 1VHR.
DR MGD; MGI:1934928; Dusp15.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
KW Alternative splicing; Hydrolase; Protein phosphatase.
FT DOMAIN 65 -125 Protein-tyrosine phosphatase.
FT ACT_SITE 88 88 Phosphocysteine intermediate (By
FT similarity).
FT VARSPLIC 88 105 CFAGISRSTTIVAYVMT -> WPLKHECRARSLSLQCS
FT (in isoform 2).
FT VARSPLIC 106 125 /FTID=VSP_007294.
FT NON_TER 125 Missing (in isoform 2).
FT NON_TER 125 /FTID=VSP_007295.
SQ SEQUENCE 125 AA; 13797 MW; D79F87FF0120F816 CRC64;

Query Match 43.1%; Score 420; DB 1; Length 125;
Best Local Similarity 56.0%; Pred. No. 5.4e-33;
Matches 70; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MNGMGNKILPGLYIGNFKDARDABQLSKNKKVTHILSVHDSARPMLGVKYLICIPAADSPS 60
Db 1 MNGMGNKILPGLYIGNFKDARDABQLSKNKKVTHILSVHDSARPMLGVKYLICIPAADSPS 60
QY 61 QNLTFRFKESIKFTHECRLGESCLVHCLAGVSRVTLVIAYIMVTDFGWEDALHTVRA 120
Db 61 VPIKKHFKECVHFTHSCRLNGNCLVHCFAGISRSTTIVAYVMTVTGLGHWQEVLEAIKA 120
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QY 121 GRSCA 125
Db 121 SRPIA 125

RESULT 14
Q86F24 PRELIMINARY; PRT; 201 AA.
ID Q86F24
AC Q86F24;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCY-2003 (TReMBLrel. 25, Last annotation update)
DE Clone Z2D1174 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22873925; PubMed=12973349; DOI=10.1038/ngl236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RT complementary DNA resource.";
RL Nat. Genet. 35:139-147(2003).
DR EMBL; AY223040; AAP06063.1; -.
DR HSSP; Q16828; 1MKP.
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 201 AA; 22013 MW; F4JACCSA4C1D85B7 CRC64;

Query Match 30.5%; Score 297; DB 2; Length 201;
Best Local Similarity 40.8%; Pred. No. 9.8e-21;
Matches 69; Conservative 28; Mismatches 66; Indels 6; Gaps 4;

QY 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKNVTHILSV-HDSARPMLEGVKYLCPAADSP 59
Db 1 MGSMSKIVPLGYGVGASQSKQLDENGITHVCVSLHYNFK--CPSRKQIILRADDD 58
QY 60 SONLTRHFKEIKETIHECRIGESCLVHCAGVRSVTLVIAYIMVTDFGWEDALHTVR 119
Db 59 KENTAKYFRDACFFIHEARVYNGAVLVCACGVRSVTLVIAYIMVTNMPPLKLVRAV 118
QY 120 AGRSCANPNVGFQLOFEKX-EVHQYRWLKEEYGESPLQ--DABEA 165
Db 119 GARPCACPNSGFLEQIEFGKSGAAKVRQELIAYYGWPKELDADIA 167

RESULT 15
ID Q86JT3 PRELIMINARY; PRT; 476 AA.
AC Q86JT3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Similar to dual-specificity protein phosphatase; protein id:
DE Act3g23610.1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AX4;
RC MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RX Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,

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RA Lehmann R., Baumgart C., Parra G., Parra J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; AAO51441.1; -.
DR HSSP; Q16828; 1MKP.
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 476 AA; 53798 MW; FFAF47417971D26F CRC64;

Query Match 26.6%; Score 259; DB 2; Length 476;
Best Local Similarity 34.2%; Pred. No. 1.4e-16;
Matches 55; Conservative 35; Mismatches 57; Indels 14; Gaps 4;

QY 2 GNGMKNILPG-----LYIGNFKDARDAEQLSKNKNVTHILSVH---DSARPMLEGVKYL 52
Db 201 GGGGSQLYPSFIIKDFLYLGAENAGNRQQLINKITHLVNAGELDDVYPHL--YKYR 258
QY 53 IPAADSPSONLTRHFKEIKETIHECRIGESCLVHCAGVRSVTLVIAYIMVTDFGWE 112
Db 259 ANLDDRPKANIYEHFEFVIQFINDCCKQGRVLHCAMGISRSVTVLAYLMKEDHMTYS 318
QY 113 DALHTVRAGRSCANPNVGFQLOFEKXPEKHEVHQYRWLKEE 153
Db 319 DAFTFCQKRSCLNPNFGVQLKDYQOHLT---LEWEKQE 356

Search completed: July 21, 2005, 19:02:21
Job time : 336 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2005, 18:05:42 ; Search time 65 Seconds
(without alignments)
272.367 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MNGMKNKILPGLYGNFKDA.....AKNLAAPGILKFWAFLLRL 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240	24.6	619	2 T15969	hypothetical prote
2	238.5	24.5	365	2 T32494	hypothetical prote
3	237.5	24.4	330	2 T39698	protein tyrosine p
4	234	24.0	223	2 I49365	protein tyrosine p
5	229.5	23.5	276	2 T48906	protein-tyrosine-p
6	224	23.0	205	2 I49364	protein tyrosine p
7	221.5	22.7	384	1 I38890	dual specificity p
8	218	22.4	866	2 F88481	protein C16A3.1 [1
9	210.5	21.6	220	2 JC7885	low-molecular-mass
10	203.5	20.9	303	2 T46405	hypothetical prote
11	203.5	20.9	393	2 A56947	dual specificity p
12	201.5	20.7	142	2 T03074	dual specificity p
13	201.5	20.7	394	2 A56115	dual specificity p
14	195.5	20.1	314	1 A57126	dual specificity p
15	194.5	19.9	367	1 S29090	dual specificity p
16	190.5	19.5	186	2 T16056	hypothetical prote
17	190.5	19.5	314	2 B57126	dual specificity p
18	189	19.4	185	1 A47196	dual specificity p
19	185.5	19.0	367	1 S24411	dual specificity p
20	185.5	19.0	367	2 S2265	dual specificity p
21	184.5	18.9	364	1 S31304	protein-tyrosine-p
22	176	18.1	226	2 T21380	hypothetical prote
23	175	17.9	272	2 T18915	hypothetical prote
24	169.5	17.4	171	1 QOVZHI	dual specificity p
25	166.5	17.1	171	1 A42514	dual specificity p
26	163.5	16.8	171	1 T36845	dual specificity p
27	163.5	16.8	171	2 T28522	probable dual spec
28	163.5	16.8	171	2 B72161	Jil protein - vari
29	160.5	16.5	171	1 B47452	dual specificity p

30	156.5	16.1	771	2 T47666	phosphatase-like p
31	153	15.7	272	2 T19418	hypothetical prote
32	136	13.9	283	2 G84458	probable protein p
33	135.5	13.9	600	2 T18446	hypothetical prote
34	135	13.8	580	2 T18439	hypothetical prote
35	130.5	13.4	292	2 S41012	hypothetical prote
36	125.5	12.9	489	1 S58725	dual specificity p
37	120.5	12.4	209	1 S48459	probable dual spec
38	117	12.0	204	2 T17802	hypothetical prote
39	114	11.7	169	2 T30684	probable dual spec
40	113	11.6	150	2 T21489	hypothetical prote
41	101.5	10.4	807	1 S44538	probable protein-t
42	100.5	10.3	278	2 T39517	dual-specificity M
43	100.5	10.3	597	1 S43743	probable dual spec
44	98.5	10.1	430	2 E90880	probable enzymes [
45	98.5	10.1	430	2 D85738	probable enzymes y

ALIGNMENTS

RESULT 1

T15969

hypothetical protein F08B1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15969

R:Chisoe, S.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid F08B1.

A:Reference number: Z18439

A:Accession: T15969

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-619 <CHI>

A:Cross-references: UNIPROT:Q10038; EMBL:U23178; NID:G726421; PID:G726422; PIDN:AAC46719.

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F08B1.1

A:Introns: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match 24.6%; Score 240; DB 2; Length 619;

Best Local Similarity 32.9%; Pred. No. 7.2e-15;

Matches 56; Conservative 33; Mismatches 69; Indels 12; Gaps 3;

Qy	2	GNGMKNKILPGLYGNFKDAEQLSKNKVTHLSVHDSARPML---EGVKYLCPAADS	58
Db	135	GDGITLPNLYLGSQIDSLDETMLDALDISVWLNLSMTCPKVCIKEDKNFMRIPVNDS	194
Qy	59	PSONLTHFEKESIKFIHECLRGSCLVHCLAGVSRVTLVIAYIMTVDGWDALHTV	118
Db	195	YQEKLSYFPWFYEFLEKCRAGKKLIHCLAGISRSFTLAISYIMRYMKGSDDAYRYV	254
Qy	119	RAGRSANPNVGFQRLQEFEE---KHEVHQYRWLK-----EYGESPL	159
Db	255	KERRSPSPNPNFNGQLLEVENVLKHVLDYNQASRPHRMVDYGFSDL	304

RESULT 2

T32494

hypothetical protein C05B10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32494

R:Geisel, C.; Wamsley, P.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C05B10.

A:Reference number: Z21178

A:Accession: T32494

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-365 <GEI>

A:Cross-references: UNIPROT:O44128; EMBL:AF036685; PIDN:AA88308.1; GSPDB:GN00022; CESP:

A:Experimental source: strain Bristol N2; clone C05B10

C:Genetics:

A:Gene: CESP:C05B10.1

A:Map position: 4

A:Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2

Query Match 24.5%; Score 238.5; DB 2; Length 365;
Best Local Similarity 37.2%; Pred. No. 5.3e-15;
Matches 51; Conservative 28; Mismatches 55; Indels 3; Gaps 1;

Qy 7 KILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLR---GVKYLCPAADSPOQL 63
Db KLTNFLVIGNAETAKNRDVLKKYISHVINVTSLNPTFEEDPNMYLRISADDNASHNL 242

Qy 64 TRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRAGRS 123
Db TRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRAGRS 123

Qy 243 TKFPPEAISFDARRNDSACLHCLAGISRSVTICLAYLMKTEMCTMDSAYEVQKRNA 302
Db TKFPPEAISFDARRNDSACLHCLAGISRSVTICLAYLMKTEMCTMDSAYEVQKRNA 302

Qy 124 CANENVGFQRLQFEK 140
Db CANENVGFQRLQFEK 140

Qy 303 SIAPNFHMGQLTDYEK 319
Db SIAPNFHMGQLTDYEK 319

RESULT 3

T39698

protein tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39698

R:Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21870

A:Accession: T39698

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-330 <WOO>

A:Cross-references: UNIPROT:O13632; EMBL:AL109652; PIDN:CAB51765.1; GSPDB:GN00067

A:Experimental source: strain 972h; cosmid c17A3

C:Genetics:

A:Gene: pi041

A:Map position: 2

Query Match 24.4%; Score 237.5; DB 2; Length 330;
Best Local Similarity 35.8%; Pred. No. 5.8e-15;
Matches 58; Conservative 29; Mismatches 66; Indels 9; Gaps 3;

Qy 3 NGMNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLR--GVKYLCPAADSPPS 60
Db NDLSEISKNYLISSMKTASELVSTSDKGIDYTLSAM-SINPNLSVPQQHLWLQIEDSSS 103

Qy 61 QNLTRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db QNLTRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRA 120

Qy 104 QNLLQYFEKSNKFTAFALSKNAKVLVHCFAGISRSVTLVAAYLMKENNWNTEALSHINE 163
Db QNLLQYFEKSNKFTAFALSKNAKVLVHCFAGISRSVTLVAAYLMKENNWNTEALSHINE 163

Qy 121 GRSCANPVGFQRLQFEK-----HEVHGYRWMLKEEYCE 156
Db GRSCANPVGFQRLQFEK-----HEVHGYRWMLKEEYCE 156

Qy 164 RRGISPNANFLQRLVYFCNQLDRSLRPLFRYGD 205
Db RRGISPNANFLQRLVYFCNQLDRSLRPLFRYGD 205

RESULT 4

I49365

protein tyrosine phosphatase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49365

R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.

J. Biol. Chem. 270, 26782-26785, 1995

A:Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s

A:Reference number: I49364; MUID:96070766; PMID:7592916

A:Accession: I49365

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-223 <RES>

A:Cross-references: UNIPROT:Q60969; EMBL:U34973; NID:gl063624; PIDN:AAA87037.1; PID:gl063624

C:Genetics:

A:Introns: 168/3

F:36-174/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>

Query Match 24.0%; Score 234; DB 2; Length 223;
Best Local Similarity 36.7%; Pred. No. 7.8e-15;
Matches 54; Conservative 26; Mismatches 59; Indels 8; Gaps 3;

Qy 1 MGNMKNILPGLYIGNFKDARDAEQ--LSKNKVTHILSVHDS-----ARPMLEGV-KYLC 52
Db MGNMKNILPGLYIGNFKDARDAEQ--LSKNKVTHILSVHDS-----ARPMLEGV-KYLC 52

Qy 53 IPAADSPQNLTRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWE 112
Db IPAADSPQNLTRHPKESIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWE 112

Qy 85 LDADNPVENIIRFFPMTEKFDGSLQNGGKLVHGNAGISRSAAAFVIAYIMETFGMKYR 144
Db LDADNPVENIIRFFPMTEKFDGSLQNGGKLVHGNAGISRSAAAFVIAYIMETFGMKYR 144

Qy 113 DALHTVRAGRS CANPVGFQRLQFEK 139
Db DALHTVRAGRS CANPVGFQRLQFEK 139

Qy 145 DAFAYQERRFCINPNAGFVHQLQEYE 171
Db DAFAYQERRFCINPNAGFVHQLQEYE 171

RESULT 5

T48906

protein-tyrosine-phosphatase (EC 3.1.3.48) [imported] - Chlamydomonas eugametos

C:Species: Chlamydomonas eugametos

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T48906

R:Haring, M.A.; Siderius, M.; Joank, C.; Hirt, H.; Walton, K.M.; Musgrave, A.

Plant J. 7, 981-988, 1995

A:Title: Tyrosine phosphatase signalling in a lower plant: cell-cycle and oxidative stres

A:Reference number: Z25005; MUID:95323001; PMID:7599654

A:Accession: T48906

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-276 <HAR>

A:Cross-references: UNIPROT:Q39491; EMBL:X77938; NID:g992593; PIDN:CAA54910.1; PID:g992593

A:Experimental source: strain UTEX 10

C:Genetics:

A:Gene: VH-PTP13

C:Keywords: phosphoric monoester hydrolase

Query Match 23.5%; Score 229.5; DB 2; Length 276;
Best Local Similarity 35.9%; Pred. No. 2.7e-14;
Matches 55; Conservative 25; Mismatches 66; Indels 7; Gaps 3;

Qy 8 ILPG-LYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLR--GVKYLCPAADSPPQNLTR 65
Db ILPG-LYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLR--GVKYLCPAADSPPQNLTR 65

Qy 90 IVPGLILSSCEVESESELTLKLGVTILQVGEELKPSHPGRTYLSLPILDMEGQDIVA 149
Db IVPGLILSSCEVESESELTLKLGVTILQVGEELKPSHPGRTYLSLPILDMEGQDIVA 149

Qy 66 HFKEKIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRAGRS 125
Db HFKEKIKPIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRAGRS 125

Qy 150 LLPSCFQLQQAQASGGVCLVHCLAGISRSASVVIAYIMTQGMPTTEARAVRRRSKV 209
Db LLPSCFQLQQAQASGGVCLVHCLAGISRSASVVIAYIMTQGMPTTEARAVRRRSKV 209

Qy 126 NPNVGFQRLQFEKHEVHGYRWMLKEEYCE 158
Db NPNVGFQRLQFEKHEVHGYRWMLKEEYCE 158

Qy 210 YPMTGFTLQLQELDRLRRESGAIQW-----GDTTP 237
Db YPMTGFTLQLQELDRLRRESGAIQW-----GDTTP 237

RESULT 6

I49364

protein tyrosine phosphatase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Mar-2004

C:Accession: I49364

R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.

J. Biol. Chem. 270, 26782-26785, 1995

A:Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s

A:Reference number: I49364; MUID:96070766; PMID:7592916

A:Accession: I49364

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-205 <RES>

A:Cross-references: EMBL:U34973; NID:gl063624; PIDN:AA87036.1; PID:gl063625
F:36-174/Domain: Vhl-type dual specificity phosphoprotein phosphatase homology <Vhl>

Query Match 23.0%; Score 224; DB 2; Length 205;
Best Local Similarity 32.8%; Pred. No. 6.4e-14;
Matches 57; Conservative 28; Mismatches 67; Indels 22; Gaps 5;

Qy 1 MGNMKNILPGLYIGNFKDARDABQ--LSKNKVTHLSVHDS-----ARPMLEGV-KYLC 52
Db 25 MRREMOEVLPLGLPGYSSAMKSLPILOKHGITHICIRQNIENAFIKPNFQQLRYLV 84
Qy 53 IPADSPSONLTHFKESIKIHEICRLRGESCLVHCLAGVSRSTLVIAIYIMTVDFGWE 112
Db 85 LDADNPVENIIRFPMTKEPIDGSLQNGKGVLVHGNAGISRSAAFPVIAYIMETFGMKYR 144
Qy 113 DALHTVAGRCANPNVGFQRLQEFKEHVEHYQVWMLKEEYGES---PLQDAE 163
Db 145 DAFYVQERRFCINPAGF-----VHQLQMLSWNSARSAPLPKQK 187

RESULT 7

I38890
dual specificity phosphoprotein phosphatase (EC 3.1.1.3 -) 5 - human
N:Alternate names: dual specificity phosphatase B23; dual specificity phosphatase hvh-3;
C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38890; A55313
R:Kwak, S.P.; Dixon, J.E.

J. Biol. Chem. 270, 1156-1160, 1995
A:Title: Multiple dual specificity protein tyrosine phosphatases are expressed and regulated by serum stimulation and heat shock
A:Reference number: A55432; MUID:95138103; PMID:7836374

A:Accession: I38890

A:Molecule type: mRNA

A:Residues: 1-384 <RES>

A:Cross-references: UNIPROT:Q16690; EMBL:U16996; NID:9642012; PIDN:AA806261.1; PID:9642012
A:Experimental source: placenta
R:Ishibashi, T.; Bottaro, D.P.; Michieli, P.; Kelley, C.A.; Aaronson, S.A.

J. Biol. Chem. 269, 29897-29902, 1994

A:Title: A novel dual specificity phosphatase induced by serum stimulation and heat shock
A:Reference number: A55313; MUID:95050849; PMID:7961985

A:Accession: A55313

A:Molecule type: mRNA

A:Residues: 1-8, 'GHV', 12-70, 'R', 72-104, 'F', 107-362, 'RCILPTQSSSABALWQRNPAPKTGMEEAQAQPOEQL
A:Cross-references: GB:U15932; NID:9606971; PIDN:AAA64693.1; PID:9606972

A:Experimental source: mammary epithelial cells

C:Genetics:

A:Gene: GDB:DUSP5

A:Cross-references: GDB:385447

A:Map position: 10q25-10q25

C:Superfamily: dual specificity phosphoprotein phosphatase 1; Vhl-type dual specificity phosphoprotein; phosphoric monoester hydrolase
F:186-317/Domain: Vhl-type dual specificity phosphoprotein phosphatase homology <Vhl>
F:265/Active site: Cys (phosphocysteine intermediate) #status predicted
F:265/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.7%; Score 221.5; DB 1; Length 384;
Best Local Similarity 36.5%; Pred. No. 2.4e-13;
Matches 50; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 4 GNMKILPGLYIGNFKDARDABQLSKNKVTHLSV-HDSARPMLEGVKYLICIPAADSPSQN 62
Db 178 GPVEILPPLYLGSAYHASKCEFLANLHITALLNVSRRTSEACMTHLVKPIWVEDSHTD 237

Qy 63 LTRHFKESIKIHEICRLRGESCLVHCLAGVSRSTLVIAIYIMTVDFGWEALHTVAGR 122
Db 238 ISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTKQFLKAEAFDIKQR 297

Qy 123 SCANPNVGFQRLQEF 139
Db 298 SWVSPNFGFMQLQIYE 314

RESULT 8

F88481

protein C16A3.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: F88481

R:anonymous, the C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F88481

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-866 <STO>

A:Cross-references: GB:chr_III; PIDN:AA847600.1; PID:gi109830; GSPDB:GN00021; CESP:C16A3

C:Genetics:

A:Gene: C16A3.1

A:Map position: 3

Query Match 22.4%; Score 218; DB 2; Length 866;

Best Local Similarity 28.5%; Pred. No. 1.4e-12;

Matches 49; Conservative 41; Mismatches 70; Indels 12; Gaps 3;

Qy 5 MNKILPGLYIGNFKDARDABQLSKNKVTHLSVHD-----SARPMLEGVKYLICIPAAD 57
Db 44 ISEILPNLILSGRTVSQNSSELLKEKNITTVINSDREVWVYNNKQKFIKNYRFYAM--SD 101

Qy 58 SPSONLTHFKESIKIHEICRLRGESCLVHCLAGVSRSTLVIAIYIMTVDFGWEALHT 117
Db 102 TASAKFDGIIIEAVRIIHDSRSKEEGLVHCFGLGVSRSATLVAFYLSALSINNRDADF 161

Qy 118 VRAGRCANPNVGFQRLQEFKEHVEHYQVWMLKEEYGESPLQDAEAKNTIL 169
Db 162 IHRFRSANPNFGFHLQKLVYSTTAKFRNQL---ISERCLRMRESKDII 210

RESULT 9

JC7885

low-molecular-mass dual-specificity phosphatase-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004

C:Accession: JC7885

R:Nakamura, K.; Tanoue, K.; Satoh, T.; Takekawa, M.; Watanabe, M.; Shima, H.; Kikuchi, K.

J. Biochem. 132, 463-470, 2002

A:Title: A novel low-molecular-mass dual-specificity phosphatase, LDP-2, with a naturally
A:Reference number: JC7885; MUID:22194259; PMID:12204117

A:Accession: JC7885

A:Molecule type: mRNA

A:Residues: 1-220 <NAK>

A:Cross-references: UNIPROT:Q99N12; DDBJ:AB038769; DDBJ:AB038770

C:Comment: This enzyme, a novel member of the low-molecular-mass dual-specificity phosphatase kinase signaling.

C:Genetics:

A:Gene: ldp-2

Query Match 21.6%; Score 210.5; DB 2; Length 220;
Best Local Similarity 36.8%; Pred. No. 1.4e-12;

Matches 49; Conservative 22; Mismatches 61; Indels 1; Gaps 1;

Qy 8 ILPLGYIGNFKDARDABQLSKNKVTHLSV-HDSARPMLEGVKYLICIPAADSPSQNLTRH 66
Db 68 IKPWLILGSDAHDLELLRGKHTILNVAYGVENAFLEFTYKTSILDVPETNLSY 127

Qy 67 FKESIKIHEICRLRGESCLVHCLAGVSRSTLVIAIYIMTVDFGWEALHTVTRAGCAN 126
Db 128 FPECFEIEQAKLDGVLVHCVNAGVSRAAAIVGFLMSSEATFTTALSUVKEARPSIC 187

Qy 127 PNVCFORQLQEF 139
Db 188 PNPGFMEQLRTYQ 200

RESULT 10

T46405
hypothetical protein DKFPz43401321.1 - human
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46405
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
A;Accession: T46405
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-303 <AAA>
A;Cross-references: UNIPROT:Q9NSW1; EMBL:AL137704
A;Experimental source: adult testis; clone DKFPz43401321
C;Genetics:
A;Note: DKFPz43401321.1

Query Match 20.9%; Score 203.5; DB 2; Length 303;
Best Local Similarity 36.4%; Pred. No. 9.3e-12;
Matches 51; Conservative 24; Mismatches 58; Indels 7; Gaps 3;

Qy 4 GNMKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLG-VKYLCTPAADSPSQN 62
Db 104 GPVEILPFLYLGSAVHAARDMLDGLITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 163
Qy 63 LTRHFESIKFI---HECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119
Db 164 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAILMVKRVRLEAEFVK 220
Qy 120 AGRSCANPNVGFQRLQEF 139
Db 221 QRRSIISFNFSFMGQLLQFE 240

RESULT 11

A56947
dual specificity phosphatase (EC 3.1.3.-) HVH2 - rat
N;Alternate names: mitogen-activated protein kinase phosphatase 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-1999
C;Accession: A56947
R;Miera-Press, A.; Rim, C.S.; Yao, H.; Roberson, M.S.; Stork, P.J.S.
J. Biol. Chem. 270, 14587-14596, 1995
A;Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression, and
A;Reference number: A56947; MUID:95301550; PMID:7782322
A;Accession: A56947
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-393 <MTS>

C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;202-333/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F;279/Active site: Cys (phosphocysteine intermediate) #status predicted
F;295/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.9%; Score 203.5; DB 2; Length 393;
Best Local Similarity 36.4%; Pred. No. 1.3e-11;
Matches 51; Conservative 24; Mismatches 58; Indels 7; Gaps 3;

Qy 4 GNMKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLG-VKYLCTPAADSPSQN 62
Db 194 GPVEILPFLYLGSAVHAARDMLDGLITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 253
Qy 63 LTRHFESIKFI---HECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119
Db 254 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAILMVKRVRLEAEFVK 310
Qy 120 AGRSCANPNVGFQRLQEF 139
Db 311 QRRSIISFNFSFMGQLLQFE 330

RESULT 12

T03074
dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03074
R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693; PMID:9482589
A;Accession: T03074
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-142 <BAH>
A;Cross-references: UNIPROT:O55737; EMBL:AF003534; NID:G2738385; PIDN:AAB94448.1; PID:G2738385

Query Match 20.7%; Score 201.5; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 5.8e-12;
Matches 48; Conservative 25; Mismatches 58; Indels 13; Gaps 2;

Qy 7 KIILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGKVYLCTPAADSPSQNLTRH 66
Db 5 KIVENLYLGNIGIRHSNYGFKIILNTRFNQ-----YGIPTVWINIDDSSESDLYSH 59
Qy 67 FKESIKFIHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVRAGRSCAN 126
Db 60 LQVTTLLIHDSIENGKVLVHCQAGISRSATVVIAYIMRSKRYSLQDAFNVKKRSIIF 119
Qy 127 PNVGFQRLQEFKEVHQYRWL 150
Db 120 PNAGFIKQLAQFER-----WL 135

RESULT 13

A56115
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 4 - human
N;Alternate names: dual specificity phosphatase HVH2
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56115
R;Guan, K.L.; Butch, E.
J. Biol. Chem. 270, 7197-7203, 1995
A;Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, which
A;Reference number: A56115; MUID:95221370; PMID:7535768
A;Accession: A56115
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-394 <GUA>
A;Cross-references: UNIPROT:Q13649; GB:U21108
C;Genetics:

A;Gene: GDB:DUSP4; HVH2; MKP-2
A;Cross-references: GDB:433893
C;Map position: 8p21-8p11.2
C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;203-334/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>
F;280/Active site: Cys (phosphocysteine intermediate) #status predicted
F;286/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.7%; Score 201.5; DB 2; Length 394;
Best Local Similarity 36.4%; Pred. No. 2e-11;
Matches 51; Conservative 23; Mismatches 59; Indels 7; Gaps 3;

Qy 4 GNMKILPGLYGNFKDARDAEQLSKNKKVTHILSVHDSARPMLG-VKYLCTPAADSPSQN 62
Db 195 GPVEILPFLYLGSAVHAARDMLDGLITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 254
Qy 63 LTRHFESIKFI---HECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119
Db 255 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAILMVKRVRLEAEFVK 311
Qy 120 AGRSCANPNVGFQRLQEF 139

Db 312 QRRSIISPNFSGQLLOFE 331

RESULT 14

A57126

dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human
N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activate
C:Species: Homo sapiens (man)
C:Date: 03-Nov-1995 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A57126
R:Rohan, P.J.; Davis, P.; Moekaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Kell
Science 259, 1763-1766, 1993
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.
A:Reference number: A57126; MUID:93206122; PMID:7681221
A:Accession: A57126
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-314 <ROH>
A:Cross-references: UNIPROT:Q05923; GB:L11329; NID:9559539; PIDN:AAA50779.1; PID:g292376
C:Genetics:
A:Gene: GDB:DUSP2
A:Cross-references: GDB:139200
A:Map position: 2q11-2q11
C:Function:
A:Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHI-type dual specificity
C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase
F:140-160/Region: nuclear location signal
F:180-311/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>
F:257/Active site: Cys (phosphocysteine intermediate) #status predicted
F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.1%; Score 195.5; DB 1; Length 314;

Best Local Similarity 34.3%; Pred. No. 5.6e-11;

Matches 47; Conservative 26; Mismatches 63; Indels 1; Gaps 1;

Qy 4 GMNKLPGLYIGNPKDARDASQLSKNKHVTHLSVHDSARPMLGV-KYLCIPAAADSPSQN 62

Db 172 GPVEILPYFLGSGSHSSDLQGLQACGITAVLNVSASCPNHFEGLYRYSIPVEDNQWVE 231

Qy 63 LTRHFKESIKPIHECRLRGSCSLVHCLAGVSRSTLVIAIYIMTVTDFGWEDALHTVRAGR 122

Db 232 ISAWFQEAIGFDWYKNSGGRLVHVCQAGISRSATICLAYLMQSRRLVRLDEAFDFVKQR 291

Qy 123 SCANPNVGFQRLQOFE 139

Db 292 GVISPNFSGQLLOFE 308

RESULT 15

S29090

dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human
N:Alternate names: protein-tyrosine-phosphatase CL100; protein-tyrosine-phosphatase, non
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C:Accession: S29090; A53052
R:Keyse, S.M.; Emalie, E.A.
Nature 359, 644-647, 1992
A:Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyrosine
A:Reference number: S29090; MUID:93024952; PMID:1406996
A:Accession: S29090
A:Molecule type: mRNA
A:Residues: 1-367 <KEY>
A:Cross-references: UNIPROT:P28562; EMBL:X68277; NID:g29980; PIDN:CAA48338.1; PID:g29981
R:Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.
J. Biol. Chem. 269, 3596-3604, 1994
A:Title: Isolation and characterization of a human dual specificity protein-tyrosine pho
A:Reference number: A53052; MUID:94148864; PMID:8106404
A:Accession: A53052
A:Molecule type: DNA
A:Residues: 1-367 <KWA>
A:Experimental source: leukocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804,

C:Genetics:

A:Gene: GDB:DUSP1; PTFN10

A:Cross-references: GDB:I36197; OMIM:600714

A:Map position: 5q34-5q34

C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHI-type dual specificity
C:Keywords: heat shock; phosphoprotein; phosphoric monoester hydrolase; stress-induced p
F:181-312/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>
F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.9%; Score 194.5; DB 1; Length 367;

Best Local Similarity 33.6%; Pred. No. 8.4e-11;

Matches 46; Conservative 25; Mismatches 65; Indels 1; Gaps 1;

Qy 4 GMNKLPGLYIGNPKDARDASQLSKNKHVTHLSVHDSARPMLGV-KYLCIPAAADSPSQN 62

Db 173 GPVEILPYFLGSAHYASRKDMLDGLGITALINVSANCPNHFEGHYQYKSIPIVEDNHKAD 232

Qy 63 LTRHFKESIKPIHECRLRGSCSLVHCLAGVSRSTLVIAIYIMTVTDFGWEDALHTVRAGR 122

Db 233 ISSWFNEAIDFIDSINKAGGRVHVHCQAGISRSATICLAYLMRTNRVVKLDEAFDFVKQR 292

Qy 123 SCANPNVGFQRLQOFE 139

Db 293 SVISPNFSGQLLOFE 309

Search completed: July 21, 2005, 19:03:32

Job time : 66 secs

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OM protein - protein search, using sw model

Run on: July 21, 2005, 18:56:44 ; Search time 91 Seconds
(without alignments)
150,939 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNMKNILPGLYIGNFKDA.....AKNIIAAPGILKFWAFLLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pap.*
 - 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pap.*
 - 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pap.*
 - 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pap.*
 - 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap.*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246.5	25.3	170	4	US-09-557-921-14
2	246.5	25.3	482	4	US-09-557-921-2
3	245.5	25.2	421	4	US-09-949-016-10488
4	245	25.1	207	4	US-09-270-767-44103
5	244.5	25.1	156	4	US-09-955-732A-3
6	244.5	25.1	170	4	US-09-544-716-12
7	244.5	25.1	170	4	US-09-557-921-12
8	244.5	25.1	170	4	US-09-564-357-15
9	244.5	25.1	170	4	US-09-619-380-14
10	244.5	25.1	491	4	US-09-949-016-8486
11	243.5	25.0	156	4	US-09-955-732A-5
12	234	24.0	223	4	US-09-685-833A-2
13	234	24.0	223	4	US-09-816-494-5
14	233.5	23.9	156	4	US-09-955-732A-4
15	233.5	23.9	168	4	US-09-544-716-13
16	233.5	23.9	168	4	US-09-557-921-13
17	233.5	23.9	168	4	US-09-564-357-16
18	233.5	23.9	168	4	US-09-619-380-15
19	228.5	23.4	659	4	US-09-955-732A-2
20	225.5	23.1	471	4	US-09-955-732A-21
21	225	23.1	172	4	US-09-704-139-5
22	225	23.1	172	4	US-09-816-494-8
23	221.5	22.7	154	4	US-09-955-732A-10
24	221.5	22.7	171	4	US-09-544-716-18
25	221.5	22.7	171	4	US-09-557-921-19
26	221.5	22.7	171	4	US-09-564-357-21
27	221.5	22.7	171	4	US-09-619-380-20

28	221.5	22.7	210	4	US-09-949-016-10939	Sequence 10939, A
29	221.5	22.7	384	4	US-09-949-016-6494	Sequence 6494, Ap
30	221.5	22.7	397	2	US-08-990-379-8	Sequence 8, Appli
31	220	22.6	155	4	US-09-955-732A-6	Sequence 6, Appli
32	220	22.6	170	4	US-09-544-716-14	Sequence 14, Appl
33	220	22.6	220	4	US-09-557-921-15	Sequence 15, Appl
34	220	22.6	170	4	US-09-564-357-17	Sequence 17, Appl
35	220	22.6	170	4	US-09-619-380-16	Sequence 16, Appl
36	220	22.6	661	4	US-09-949-016-9121	Sequence 9121, Ap
37	217.5	22.3	283	4	US-09-270-767-45300	Sequence 45300, A
38	217.5	22.3	737	4	US-09-955-732A-13	Sequence 13, Appl
39	216.5	22.2	173	4	US-09-704-139-4	Sequence 4, Appli
40	216.5	22.2	173	4	US-09-816-494-7	Sequence 7, Appli
41	212	21.7	174	4	US-09-544-716-20	Sequence 20, Appl
42	212	21.7	211	4	US-09-544-716-2	Sequence 2, Appli
43	210.5	21.6	552	4	US-09-955-732A-15	Sequence 15, Appl
44	208	21.3	665	4	US-09-816-494-2	Sequence 2, Appli
45	206.5	21.2	299	4	US-09-564-357-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-557-921-14
; Sequence 14, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-14

Query Match 25.3%; Score 246.5; DB 4; Length 170;
Best Local Similarity 38.6%; Pred. No. 4.2e-22;
Matches 54; Conservative 29; Mismatches 52; Indels 5; Gaps 2;

Qy	5	MNKLPGLYIGNFKDARDAEOLSKNKNVTHLSVHDSARPMLEGVK----	YLCIPADSPS 60
Db	27	LTPILPFLGNEQDAQDLTMQRLNIGYVINV-TTHPLVHYBKGLFNFKRLPATDSNK 85	
Qy	61	QNLTRHFKESIKFTHECRLCGESCLVHCLAGSVSVTLVIAYINTVTDGFWEDALHTVRA 120	
Db	86	QNLQYFEAEFEFEHAHQCGKGLLIHCQAGVSATIVIALMKHTMTWTDAYKFKVG 145	
Qy	121	GRSCANPNVGFQRLQBFKEK 140	
Db	146	KRPIISPNLPMGQLLEFEE 165	

RESULT 2
US-09-557-921-2
; Sequence 2, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-2

Query Match      25.3%; Score 246.5; DB 4; Length 482;
Best Local Similarity 38.6%; Pred. No. 2.1e-21;
Matches 54; Conservative 29; Mismatches 52; Indels 5; Gaps 2;

Qy 5 MNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVK---YLCIPAAADSPS 60
Db 322 LTPILPFLFLNGEQDQLDQMLRNIGWINV--FTPLPHYEKGLFPNFKRLPATDSNK 380

Qy 61 QNLTRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 381 QNLQYFEEAFEEAFEEAHQCCKGLLIHCQAGVSRSATIVIAIYLMKTRMTMTDAYKFKYK 440

Qy 121 GRSCANPNVGFQRLQEFK 140
Db 441 KRPIISNLFNFMGQLLEFEE 460

RESULT 3
US-09-949-016-10488
; Sequence 10488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10488
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10488

Query Match      25.2%; Score 245.5; DB 4; Length 421;
Best Local Similarity 39.6%; Pred. No. 2.2e-21;
Matches 59; Conservative 24; Mismatches 59; Indels 7; Gaps 2;

Qy 7 KILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLE---GVKYLCPAADSPSONL 63
Db 243 QILPNLYGSARDSANLESIAKLGIRYILNVTPLNPFNFEEKNGDFHYKQIPISDHWSONL 302

Qy 64 TRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 123
Db 303 SRFPPEALEFIDEALSQNGVYLHCLAGVSRSVTTVAYILMQKLHLSLNDAYDLVGRKKS 362

Qy 124 CANPNVGFQRLQEFK---HEVHQVQ 148
Db 363 NISNPNFMGQLDPERSLRLEERHSQEQ 391

RESULT 4
US-09-270-767-44103
; Sequence 44103, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
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; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44103
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44103

Query Match      25.1%; Score 245; DB 4; Length 207;
Best Local Similarity 42.3%; Pred. No. 8.7e-22;
Matches 58; Conservative 20; Mismatches 55; Indels 4; Gaps 3;

Qy 7 KILPG-LYIGNFKDARDAEQLSKNKVTHILSV-HDSARPMLE---VKYLCIPAAADSPSON 62
Db 13 EIIPGLFLGNATHSCDSEALKKYNIKYVLNVTPDLPNKFKESGDIKYLOIPITDHYSON 72

Qy 63 LTRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 122
Db 73 LAIHFPDAIOFIEARSASSVVLVHCLAGVSRSVTLVIAYLMHTRGLSLNDAFANVDRDK 132

Qy 123 SCANPNVGFQRLQEFK 139
Db 133 PDVSPNPFHFMQLLSPE 149

RESULT 5
US-09-955-732A-3
; Sequence 3, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-3

Query Match      25.1%; Score 244.5; DB 4; Length 156;
Best Local Similarity 41.0%; Pred. No. 6.6e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGV---KYLCPAADSPSONL 63
Db 15 EIIPFLYLGCADSTNLDVLEEFGIKYLNVTPNLNLFENAGEFKYKQIPISDHWSONL 74

Qy 64 TRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 121
Db 75 SQFPEAISFIDEA--RGKNCGVLVHCLAGISRVTTVAYILMQKLNSMNDAYDIVMKK 132

Qy 122 RSCANPNVGFQRLQEFK 140
Db 133 KSNISPNFNFMGQLDPER 151

RESULT 6
US-09-544-716-12
; Sequence 12, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-12

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNPKDARDAEQLSKNKKVTHLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCARDSTNLDVLEEFGIKYLNTVTPNLPLNFENAGFKYKQIPISDHWSQNL 87
Qy 64 TRHPKESIKFTHECLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDFGWEDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVOMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFQQLLDFER 164

RESULT 7
US-09-557-921-12
; Sequence 12, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-12

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNPKDARDAEQLSKNKKVTHLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCARDSTNLDVLEEFGIKYLNTVTPNLPLNFENAGFKYKQIPISDHWSQNL 87
Qy 64 TRHPKESIKFTHECLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDFGWEDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVOMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFQQLLDFER 164

RESULT 8
US-09-564-357-15
; Sequence 15, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-15

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNPKDARDAEQLSKNKKVTHLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCARDSTNLDVLEEFGIKYLNTVTPNLPLNFENAGFKYKQIPISDHWSQNL 87
Qy 64 TRHPKESIKFTHECLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDFGWEDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVOMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFQQLLDFER 164

RESULT 9
US-09-619-380-14
; Sequence 14, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-14

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNPKDARDAEQLSKNKKVTHLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCARDSTNLDVLEEFGIKYLNTVTPNLPLNFENAGFKYKQIPISDHWSQNL 87
Qy 64 TRHPKESIKFTHECLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDFGWEDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVOMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFQQLLDFER 164

RESULT 10
US-09-949-016-8486
; Sequence 8486, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6486
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8486

Query Match      25.1%; Score 244.5; DB 4; Length 491;
Best Local Similarity 41.0%; Pred. No. 3.8e-21;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

QY      7 KILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGV--KYLCPAADSPSQNL 63
DB      319 EILPFYILGCAKOSTNLDVLEEFGIKIYINVTPLNLPENAGEFYKQIPISDHWSQL 378
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY      64 TRHFKESIKFIHCELRGESC--LVHCLAGVSRSVTLVIAYIMTVTDGFWEDALHTVRAG 121
DB      379 SQFFPEAISFIDEA--RGKNCGLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMK 436
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY      122 RSCANPNVGFQRLQEFK 140
DB      437 KSNISPNFNFMGQLLDFER 455
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 11
US-09-955-732A-5
; Sequence 5, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-5

Query Match      25.0%; Score 243.5; DB 4; Length 156;
Best Local Similarity 40.9%; Pred. No. 8.7e-22;
Matches 56; Conservative 24; Mismatches 54; Indels 3; Gaps 1;

QY      7 KILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPML---GVKYLCPAADSPSQNL 63
DB      15 QILPNLYLGSARDSANLESKLGIYILNVTPLNLPNFFKNGDFHYKQIPISDHWSQL 74
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY      64 TRHFKESIKFIHCELRGESCGLVHCLAGVSRSVTLVIAYIMTVTDGFWEDALHTVRAGS 123
DB      75 SRFFPEAIEFIDBALSQNCGLVHCLAGVSRSVTVTVAYLMQKLNLSMNDAYDLVRRKKS 134
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY      124 CANPNVGFQRLQEFK 140
DB      135 NISPNFNFMGQLLDFER 151
      :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 12
US-09-685-853A-2
; Sequence 2, Application US/09685853A
; Patent No. 6479270
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,

```

```
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-4

Query Match      23.9%; Score 233.5; DB 4; Length 156;
Best Local Similarity 40.1%; Pred.No.1.5e-20;
Matches 55; Conservative 24; Mismatches 55; Indels 3; Gaps 1;

QY 7 KILPGLYIGNFKDARDABQLSKNKVTHILSVHDSARPML---GVKYLICIPAADSPSONL 63
Db 15 QILPYLYLGCAKSTNLDVLGVGKIKYILNVTPLNPAFEGGGEFTYKQIPISDHWSQNL 74
QY 64 TRHFKEISKFIHECLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVTRAGRS 123
Db 75 SQFFPEAISFIDEARSKCGVLVHCLAGISRSVTVVAYLMQKNLNLNDAYDFVKRKKS 134
QY 124 CANPNVGFQRLQEFPEK 140
Db 135 NISPNFMGQLLDFER 151
```

```
RESULT 15
US-09-544-716-13
; Sequence 13, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-13
```

```
Query Match      23.9%; Score 233.5; DB 4; Length 168;
Best Local Similarity 40.1%; Pred.No.1.7e-20;
Matches 55; Conservative 24; Mismatches 55; Indels 3; Gaps 1;

QY 7 KILPGLYIGNFKDARDABQLSKNKVTHILSVHDSARPML---GVKYLICIPAADSPSONL 63
Db 26 QILPYLYLGCAKSTNLDVLGVGKIKYILNVTPLNPAFEGGGEFTYKQIPISDHWSQNL 85
QY 64 TRHFKEISKFIHECLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVTRAGRS 123
Db 86 SQFFPEAISFIDEARSKCGVLVHCLAGISRSVTVVAYLMQKNLNLNDAYDFVKRKKS 145
QY 124 CANPNVGFQRLQEFPEK 140
Db 146 NISPNFMGQLLDFER 162
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Search completed: July 21, 2005, 19:25:06
Job time : 91 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2005, 15:47:20 ; Search time 275 Seconds
(without alignments)
258.778 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNMKNILPGLYIGNFKDA.....AKNLAAPGILKFWAFLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	184	3	Aay68795 Amino aci
2	975	100.0	184	4	Aab73216 Human pho
3	975	100.0	184	4	Aab66431 Human DSP
4	975	100.0	184	4	AAG78217 Human MAP
5	975	100.0	184	4	Aab67167 Human dua
6	975	100.0	184	5	Abb90435 Human pol
7	975	100.0	184	5	Adi16892 Human NOV
8	975	100.0	184	5	ADI17160 Human NOV
9	975	100.0	184	6	ABR43462 Human DSP
10	975	100.0	184	7	ADN75958 Human sig
11	975	100.0	184	8	ADN75954 Human sig
12	975	100.0	184	8	ADP25001 PRO polyp
13	975	100.0	190	4	AAU23521 Novel hum
14	975	100.0	190	4	AAU21668 Novel hum
15	975	100.0	190	4	AAU21796 Novel hum
16	975	100.0	190	7	ADC46309 Human neo
17	975	100.0	190	7	ADC46437 Human neo
18	959	98.4	184	6	ABR43457 Human dua
19	932	95.6	184	4	Aab73213 Murine ph
20	932	95.6	184	5	ADI17161 Murine NO
21	932	95.6	184	5	ADI16893 Murine NO
22	923	94.7	184	5	ADI16894 Human NOV
23	923	94.7	184	5	ADI17162 Human NOV
24	897	92.0	205	4	AAB81105 Human JNK
25	856	87.8	205	4	AAB66443 Murine DS

ALIGNMENTS

RESULT 1

AAy68795
ID AAY68795 standard; protein; 184 AA.

XX AC AAY68795;

XX DT 16-MAY-2000 (first entry)

XX DE Amino acid sequence of a human phosphorylation effector PHSP-27.

XX KW Human; phosphorylation effector; PHSP; proliferative disorder; immune disorder; neuronal disorder.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 36

FT Modified-site /note= "potential phosphorylation domain"

FT Modified-site 40

FT Modified-site /note= "potential phosphorylation domain"

FT Modified-site 50

FT Modified-site /note= "potential phosphorylation domain"

FT Modified-site 62

FT Modified-site /note= "potential glycosylation domain"

FT Domain 63..118

FT Modified-site /note= "tyrosine phosphatase active site domain"

FT Modified-site 70

FT Modified-site /note= "potential phosphorylation domain"

FT Modified-site 105

FT Modified-site /note= "potential phosphorylation domain"

FT Modified-site 117

FT Modified-site /note= "potential phosphorylation domain"

XX WO200006728-A2.

XX PD 10-FEB-2000.

XX PP 28-JUL-1999; 99WO-US017132.

XX PR 28-JUL-1998; 98US-0155213P.

XX PR 14-SEP-1998; 98US-0155196P.

XX PR 14-OCT-1998; 98US-0155239P.

XX PR 03-NOV-1998; 98US-0106889P.

XX PR 19-NOV-1998; 98US-0109033P.

XX PR 22-DEC-1998; 98US-0113796P.

XX PR 12-JAN-1999; 99US-0155233P.

XX PA (INCY-) INCYTE PHARM INC.

26 843 86.5 205 4 AAB81106
27 825.5 84.7 167 3 AAB23298
28 758.5 77.8 145 4 AAB66442
29 673 69.0 162 7 ADB65317
30 540 55.4 122 4 AAU23718
31 528 54.2 235 5 AAE22996
32 528 54.2 235 5 ADI16890
33 528 54.2 235 5 ADI17159
34 528 54.2 235 6 ABR43456
35 528 54.2 235 6 ABR43461
36 528 54.2 235 8 ADN76006
37 528 54.2 235 8 ADN75958
38 528 54.2 289 5 AAE22997
39 528 54.2 289 6 ABR43462
40 528 54.2 329 4 AAE04840
41 528 54.2 329 5 AAU75792
42 528 54.2 329 6 ABR43460
43 521 53.4 236 5 ADI16572
44 512 52.5 236 8 ADN42226
45 483.5 49.6 149 6 ABR43466

Aab81106 Murine JN
Aab23298 Human dua
Aab66442 Human MAP
Adb65317 Human pro
Aau23718 Novel hum
Aae22996 Human pro
Adi16890 Human NOV
Adi17159 Human NOV
Abr43456 Human dua
Abr43461 Human DSP
Adn76006 Human DSP
Adn75958 Human sig
Aae22997 Human pro
Abr43462 Human DSP
Aae04840 Human SGP
Aau75792 Human pro
Abr43460 Human DSP
Adi16572 Human NOV
Adn42226 Human nov
Abr43466 Multiple

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;
 PI Reddy R, Lu DAM, Shih LL;
 XX WPI: 2000-183125/16.
 DR N-PSDB; AAZ46164.
 XX New human phosphorylation effectors useful for the diagnosis, treatment
 PT and prevention of proliferative, immune and neuronal disorders.
 XX
 PS Claim 1; Page 114-115; 142pp; English.
 XX
 CC AAY68769-95 and AAY68797-99 represent human phosphorylation effectors
 CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not
 CC given in the specification). The sequences were isolated from cDNA
 CC libraries prepared from various human tissues. The PHSP proteins are
 CC useful for the diagnosis, treatment and prevention of proliferative
 CC disorders, immune disorders and neuronal disorders. The PHSP proteins
 CC form pharmaceutical compositions which useful for treating or preventing
 CC disorders associated with decreased PHSP expression/activity. PHSP
 CC antagonists are useful for treating or preventing disorders associated
 CC with increased PHSP expression/activity
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 975; DB 3; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60
 QY 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120
 DB 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQRLQBFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQBFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 QY 181 LRL 184
 DB 181 LRL 184

RESULT 2
 AAB73216
 ID AAB73216 standard; protein; 184 AA.

XX AAB73216;
 AC
 XX 11-MAY-2001 (first entry)
 DT
 XX Human phosphatase AAB73216_h.
 DE
 XX Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;
 KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
 KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;
 KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
 KW schizophrenia; hamartoma.
 XX
 OS Homo sapiens.
 XX
 PN WO200112819-A2. NPA
 XX
 PD 22-FEB-2001.
 XX
 PF 11-AUG-2000; 2000WO-US022158.
 XX
 PR 13-AUG-1999; 99US-0149005P.
 .XX

PA (SUGE-) SUGEN INC.
 XX Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
 XX WPI: 2001-211226/21.
 DR N-PSDB; AAF63568.
 XX New protein phosphatase polypeptide for diagnosing and treating
 PT phosphatase related disorders such as cancer, schizophrenia, cardiac
 PT dysfunction and/or vascular disorders.
 XX
 PS Claim 6; Fig 5; 138pp; English.
 XX
 CC The present invention relates to phosphatase proteins and coding
 CC sequences. The present sequence is one such phosphatase. Phosphatases are
 CC enzymes that catalyze the dephosphorylation of proteins modified by
 CC phosphorylation of serine, threonine or tyrosine residues. The
 CC phosphatases are useful for treating a variety of diseases: for example
 CC cancer e.g. breast, urogenital, prostate, head, neck, lung cancers,
 CC synovial sarcomas, renal cell carcinoma, non-small cell lung cancer,
 CC hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer,
 CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological
 CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,
 CC congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease,
 CC ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan
 CC Zonana syndrome, schizophrenia and hamartomas
 XX

SQ Sequence 184 AA;
 Query Match 100.0%; Score 975; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60
 QY 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120
 DB 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQRLQBFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQBFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 QY 181 LRL 184
 DB 181 LRL 184

RESULT 3
 AAB66431
 ID AAB66431 standard; protein; 184 AA.

XX AAB66431;
 AC
 XX 06-APR-2001 (first entry)
 DT
 XX Human DSP-3 protein.
 DE
 XX Human; DSP-3; cytostatic; immunosuppressive; antiallergic;
 KW dual specificity phosphatase-3; cell proliferation; metabolic diseases;
 KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;
 KW autoimmune disease; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200102582-A1. NPA
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-US018207.
 XX

PR 02-JUL-1999; 99US-0142338P.
 PR 07-APR-2000; 2000WO-US009185.
 PR 20-APR-2000; 2000WO-US010868.
 XX
 PA (CEPT-) CEPTVR INC.
 XX
 PI Luche RM, Wei B;
 XX
 XX WPI; 2001-138149/14.
 DR N-PSDB; AAF29601.
 XX
 XX New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form
 PT polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate
 PT form activity, especially for treating e.g. cancer, autoimmune diseases
 PT or allergies.
 XX
 XX Claim 1; Fig 2; 86pp; English.
 PS
 XX The present sequence is given in a specification providing human dual
 CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.
 CC The polypeptides are useful for dephosphorylating a substrate of DSP-3,
 CC e.g. MAP-kinase. They may be used to treat or prevent diseases associated
 CC with cell proliferation, immunosuppression, metabolic diseases, or
 CC abnormal cell growth or cell cycle abnormalities. They are also useful
 CC for identifying agents that modulate their activity. The modulators are
 CC useful for treating disorders associated with DSP-3 or DSP-3 variant
 CC activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
 CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal
 CC cell growth, abnormal cell proliferation and cell cycle abnormalities.
 CC The modulating agents are useful for modulating, modifying or altering
 CC cellular responses, e.g. in vivo or in vitro cell proliferation,
 CC differentiation or survival
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 975; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGMKNILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGVKYLICIPAADS 60
 DB 1 MNGMKNILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGVKYLICIPAADS 60
 QY 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120
 DB 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
 QY 181 LRL 184
 DB 181 LRL 184
 RESULT 4
 AAG78217
 ID AAG78217 standard; protein; 184 AA.
 AC
 XX AAG78217;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 XX Human MAP kinase interacting kinase phosphatase x.
 DE Human; MAP kinase interacting kinase phosphatase x; hMKPx; adrenal gland.
 KW Homo sapiens.
 OS
 XX CN1301869-A.
 FN
 XX 04-JUL-2001.
 PD

XX 27-DEC-1999; 99CN-00125397.
 XX 27-DEC-1999; 99CN-00125397.
 PR
 XX (SREH-) SOUTHERN RES CENT STATE HUMAN GENE GROUP.
 XX
 XX Gu J, Peng Y, Li Y;
 XX
 XX WPI; 2001-550488/62.
 DR N-PSDB; AAI64795.
 XX
 XX New human mitogen activated protein kinase phosphatase and its code
 PT sequence.
 PT
 XX Claim 4; Fig 2; 25pp; Chinese.
 PS
 XX The invention relates to human MAP kinase-interacting kinase phosphatase
 CC x (Genbank Accession Number AF165519), shortly named hMKPx, expressed in
 CC adrenal gland tissue of normal human body and its coding sequence as well
 CC as the preparation and application of the protein and nucleic acid
 CC sequence and the method of detecting hMKPx nucleic acid sequence and
 CC polypeptide in sample
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 975; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGMKNILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGVKYLICIPAADS 60
 DB 1 MNGMKNILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGVKYLICIPAADS 60
 QY 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120
 DB 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
 QY 181 LRL 184
 DB 181 LRL 184
 RESULT 5
 AAB67167
 ID AAB67167 standard; protein; 184 AA.
 XX
 AC AAB67167;
 XX
 DT 12-APR-2001 (first entry)
 XX
 XX Human dual-specificity phosphatase DSP-3.
 DE Human; DSP-3; dual-specificity phosphatase; cell proliferation;
 KW cell signalling; cancer; graft-versus-host disease; autoimmune disease;
 KW allergy; metabolic disease; Duchenne muscular dystrophy.
 XX
 OS Homo sapiens.
 XX WO200102581-A1.
 FN
 XX 11-JAN-2001.
 PD
 XX 20-APR-2000; 2000WO-US010868.
 PF
 XX 02-JUL-1999; 99US-0142338P.
 PR 07-APR-2000; 2000WO-US009185.
 XX
 XX (CEPT-) CEPTVR INC.

NPA

NPA

XX Luche RM, Wei B;
 XX WPI; 2001-138148/14.
 DR N-PSDB; AAF32191.
 XX
 PT New dual-specificity phosphatase-3 polypeptide and its variants useful
 PT for treating disorders associated with DSP-3 activity, defects in cell
 PT proliferation, differentiation or survival, e.g. Duchenne muscular
 PT dystrophy, cancer.
 XX
 XX Claim 1; Fig 2; 70pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human dual-specificity phosphatase DSP-3. The DSP-3 protein is involved
 CC in cell signalling and the sequences can be used in the treatment of
 CC cancer, metabolic and autoimmune diseases, allergies, graft-versus-host
 CC disease, abnormal cell proliferation and Duchenne muscular dystrophy
 XX
 XX Sequence 184 AA;
 XX
 Query Match 100.0%; Score 975; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLCPAADSPPS 60
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLCPAADSPPS 60
 XX
 QY 61 QNLTRHPKESIKFTHCELRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 DB 61 QNLTRHPKESIKFTHCELRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 XX
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 XX
 QY 181 LRRL 184
 DB 181 LRRL 184
 XX
 RESULT 6
 ID ABB90435 standard; protein; 184 AA.
 AC ABB90435;
 XX
 XX 24-MAY-2002 (first entry)
 DT
 DE Human polypeptide SEQ ID NO 2811.
 XX
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200190304-A2.
 XX
 XX 29-NOV-2001.
 FD
 XX 18-MAY-2001; 2001WO-US016450.
 PF
 XX 19-MAY-2000; 2000US-0205515P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 FA
 XX Birse CE, Rosen CA;
 FI
 XX WPI; 2002-122018/16.
 DR

DR N-PSDB; ABL90844.
 XX
 PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 XX Claim 11; SEQ ID NO 2811; 2081pp + Sequence Listing; English.
 PS
 XX The invention relates to novel genes (ABL99449-ABL90853) and proteins
 CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 184 AA;
 XX
 Query Match 100.0%; Score 975; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLCPAADSPPS 60
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLCPAADSPPS 60
 XX
 QY 61 QNLTRHPKESIKFTHCELRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 DB 61 QNLTRHPKESIKFTHCELRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 XX
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 XX
 QY 181 LRRL 184
 DB 181 LRRL 184
 XX
 RESULT 7
 ID ADI16892
 XX ADI16892 standard; protein; 184 AA.
 AC ADI16892;
 XX
 XX 15-APR-2004 (first entry)
 DT
 XX Human NOVX protein homologue SeqID 428.
 DE
 XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; str.
 XX
 OS Homo sapiens.
 XX
 XX WO200268649-A2.
 XX
 XX 06-SEP-2002.
 PD
 XX 31-JAN-2002; 2002WO-US002785.
 PF

NPA

XX 31-JAN-2001; 2001US-0265395P.
 PR 31-JAN-2001; 2001US-0265412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 02-FEB-2001; 2001US-0266408P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 08-FEB-2001; 2001US-0267057P.
 PR 09-FEB-2001; 2001US-0267459P.
 PR 09-FEB-2001; 2001US-0267823P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271833P.
 PR 27-FEB-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0272788P.
 PR 02-MAR-2001; 2001US-0273048P.
 PR 14-MAR-2001; 2001US-0275923P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 14-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 15-MAR-2001; 2001US-0276450P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 16-MAR-2001; 2001US-0276768P.
 PR 20-MAR-2001; 2001US-0278652P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278778P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282922P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 (CURA-) CURAGEN CORP.
 Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
 Li L, Gangolli EA, Padigara DW, Rastelli L, Miller CE;
 Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CE;
 Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 WPI; 2002-706998/76.
 New NOVX polypeptides and nucleic acids, useful for preventing or
 treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 pharmacogenomics.
 Disclosure; SEQ ID NO 428; 1498pp; English.
 This invention relates to a novel nucleic acids, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.
 XX Sequence 184 AA;
 SQ
 Query Match 100.0%; Score 975; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNMKNILPGLYIGNFKDARDARQLSKNKKVTHILSVHDSARPMLEGVKYLICIPADSPS 60
 DB 1 MGNMKNILPGLYIGNFKDARDARQLSKNKKVTHILSVHDSARPMLEGVKYLICIPADSPS 60
 QY 61 QNLTFRHFESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 DB 61 QNLTFRHFESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQROLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQROLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 QY 181 LRRL 184
 DB 181 LRRL 184
 RESULT 8
 ADI17160
 ID ADI17160 standard; protein; 184 AA.
 XX ADI17160;
 AC ADI17160;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human NOVX protein homologue SeqID 696.
 XX
 KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (IgA) nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; str.
 XX Homo sapiens.
 OS
 XX WO200268649-A2. NPA
 FN
 XX 06-SEP-2002.
 PD
 XX 31-JAN-2002; 2002WO-US002785.
 PF
 XX

PR 31-JAN-2001; 2001US-0265395P.
 PR 31-JAN-2001; 2001US-0265412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 05-FEB-2001; 2001US-0266406P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 07-FEB-2001; 2001US-0270577P.
 PR 08-FEB-2001; 2001US-0267459P.
 PR 09-FEB-2001; 2001US-0268723P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271839P.
 PR 27-FEB-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0272788P.
 PR 02-MAR-2001; 2001US-0273046P.
 PR 14-MAR-2001; 2001US-0275925P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 14-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 15-MAR-2001; 2001US-0276450P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 16-MAR-2001; 2001US-0276768P.
 PR 20-MAR-2001; 2001US-0278652P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278778P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 20-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 PR (CURA-) CURAGEN CORP.
 XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
 PI Li L, Gangolli EA, Padigaru DW, Rastelli L, Miller CE;
 PI Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CE;
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2002-706998/76.
 DR
 XX
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Disclosure; SEQ ID NO 696; 1498pp; English.
 XX
 CC This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytoskeletal, anti-HIV, anti-diabetic, anti-arteriosclerotic, anorectic,
 CC antiasthmatic, nephrotropic, antibacterial, virucide, hepatotropic,
 CC neuroprotective, nootropic, antitaxial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.
 XX
 SQ Sequence 184 AA;
 Query Match 100.0%; Score 975; DB 5; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MNGMKNKILPGLYIGNFKDARDAEQSLSKVTHLSVHDSARPMLEGVKYLCTIPAAADSPS 60
 Db 1 MNGMKNKILPGLYIGNFKDARDAEQSLSKVTHLSVHDSARPMLEGVKYLCTIPAAADSPS 60
 Qy 61 QNLTRHPKESIKFTHCECLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWDALHTVRA 120
 Db 61 QNLTRHPKESIKFTHCECLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWDALHTVRA 120
 Qy 121 GRSCANPNVGFQRLQEFKEHVEHQVQLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 Db 121 GRSCANPNVGFQRLQEFKEHVEHQVQLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
 Qy 181 LRRL 184
 Db 181 LRRL 184
 RESULT 9
 ABR42923
 ID ABR42923 standard; protein; 184 AA.
 XX AC ABR42923;
 XX DT 08-SEP-2003 (first entry)
 XX DE Human mitogen-activated protein kinase phosphatase X (MKPX).
 XX KW Mitogen-activated protein kinase phosphatase X; MKPX; enzyme; human;
 XX KW cancer; vaccine; gene therapy; cytostatic.
 XX OS Homo sapiens.
 XX FN WO2003044161-A2. **NPA**
 XX PD 30-MAY-2003.
 XX PF 05-NOV-2002; 2002WO-US035312.
 XX PR 15-NOV-2001; 2001US-0331394P.
 XX PA (TULA-) TULARIK INC.
 XX

KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;
 KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;
 KW antidiabetic; anorectic; cancer; autoimmune disease; infection;
 KW inflammation; diabetes; obesity; RNA interference; gene silencing.
 XX Homo sapiens.
 OS
 XX WO2004016735-A2. **NPA**
 PN
 XX 26-FEB-2004.
 PD
 XX 23-MAY-2003; 2003WO-US016632.
 PF
 XX 23-MAY-2002; 2002US-0383249P.
 PR
 XX 14-APR-2003; 2003US-0462942P.
 XX
 XX (CEPT-) CEPTVR INC.
 PA
 XX (COLD-) COLD SPRING HARBOR LAB.
 PI
 XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;
 DI
 XX WPI; 2004-203773/19.
 DR
 XX N-PSDB; ADN75953.
 DR

NPA

PT New isolated small interfering RNA (siRNA) polynucleotide useful for
 PT treating diseases with aberrant activity of the protein tyrosine
 PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,
 PT diabetes and obesity.
 XX
 XX Disclosure; SEQ ID NO 779; 392pp; English.
 PS
 XX
 XX This invention describes novel small interfering RNA (siRNA)
 CC polynucleotides capable of interfering with expression of a polypeptide
 CC having protein-tyrosine-phosphatase (PTP) activity. The products of the
 CC invention have cytostatic, immunomodulator, antimicrobial,
 CC antiinflammatory, antidiabetic and anorectic activity. The methods and
 CC conditions of the present invention are useful for treating diseases or
 CC conditions associated with aberrant expression or activity of the protein
 CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,
 CC inflammation, diabetes and obesity. This sequence represents a siRNA
 CC directed against dual specificity phosphatase (DSP) expression.
 XX
 XX Sequence 184 AA;
 SQ

Query Match 100.0%; Score 975; DB 8; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPAADSPS 60
 DB 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPAADSPS 60
 QY 61 QNLTTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
 DB 61 QNLTTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
 QY 121 GRSCANPNVGFQRLQEPKEHEVHQYRWLKEEYGESPLQDAEAKNIIAAPGILKFWAF 180
 DB 121 GRSCANPNVGFQRLQEPKEHEVHQYRWLKEEYGESPLQDAEAKNIIAAPGILKFWAF 180
 QY 181 LRRLL 184
 DB 181 LRRLL 184

RESULT 12
 ADP25001
 ID ADP25001 standard; protein; 184 AA.
 XX
 AC ADP25001;
 XX
 DT 18-NOV-2004 (first entry)
 XX

DE PRO polypeptide SEQ ID NO:2179.
 XX
 KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 XX WO2004041170-A2. **NPA**
 PN
 XX 21-MAY-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034312.
 PF
 XX 01-NOV-2002; 2002US-0423394P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WL;
 PI Wu TD;
 PI
 DR WPI; 2004-419628/39.
 DR N-PSDB; ADP25000.
 DR
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 XX Claim 7; SEQ ID NO 2179; 2940pp; English.
 PS
 XX

CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 XX Sequence 184 AA;
 SQ

Query Match 100.0%; Score 975; DB 8; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPAADSPS 60
 DB 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPAADSPS 60
 QY 61 QNLTTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
 DB 61 QNLTTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120

QY 121 GRSCANPVGFQRLQEFKEKHVHOYRWLKEEYGESPLQDAERAKNLAAPGILKFWAF 180
Db 121 GRSCANPVGFQRLQEFKEKHVHOYRWLKEEYGESPLQDAERAKNLAAPGILKFWAF 180
QY 181 LRRL 184
Db 181 LRRL 184

RESULT 13
AAU23521
ID AAU23521 standard; protein; 190 AA.
XX
AC AAU23521;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human enzyme polypeptide #607.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
OS Homo sapiens.
XX
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XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI; 2001-465558/50.	
XX	N-PSDB; AAS34867.	
DR		
XX		
PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to	
PT	diagnose diseases or disorders associated with aberrant expression or	
PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis,	
XX		
PS	Claim 11; SEQ ID NO 395; 687pp; English.	
XX		
CC	The present invention relates to the isolation of novel human neoplastic	
CC	disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA	
CC	sequences encoding for these polypeptides. The sequences of the invention	
CC	are useful in the diagnosis, treatment, prevention and/or prognosis of	
CC	disorders involving neoplastic disease such as hyperproliferative	
CC	disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem	
CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or	
CC	Hodgkin's lymphoma). The sequences of the invention may also be useful	
CC	for treating other disorders such as neural disorders, immune system	
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal	
CC	disorders, pulmonary disorders, cardiovascular disorders and renal	
CC	disorders. The polynucleotide sequences of the invention are also useful	
CC	in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic	
CC	disease associated polypeptides of the invention. Note: The sequence data	
CC	for this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
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XX AC AAU21796;
DT 04-DEC-2001 (first entry)
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XX KW Human; neoplastic disease associated polypeptide; cancer;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.
XX OS Homo sapiens.
XX WO200155163-A1.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001358.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 21, 2005, 19:02:30 ; Search time 71 Seconds
(without alignments)
1006.009 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

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Total number of hits satisfying chosen parameters: 1736639

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Post-processing: Minimum Match 0%

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6	975	100.0	190	14	US-10-103-313-195
7	975	100.0	190	14	US-10-103-313-523
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9	932	95.6	184	15	US-10-072-012-429
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12	923	94.7	184	15	US-10-072-012-698	Sequence 698, App
13	897	92.0	205	17	US-10-803-738-2	Sequence 2, Appli
14	843	86.5	205	17	US-10-803-738-4	Sequence 4, Appli
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16	673	69.0	162	15	US-10-104-047-3471	Sequence 3471, Ap
17	528	54.2	235	9	US-09-963-204-2	Sequence 2, Appli
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ALIGNMENTS

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; Publication No. US20030148341A1
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; APPLICANT: SIN, Wun Chey
; APPLICANT: YANG, Jianxin
; TITLE OF INVENTION: Gene Amplification and Overexpression in Cancer
; FILE REFERENCE: 38002-0038
; CURRENT APPLICATION NUMBER: US/10/287,806
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/331,394
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-806-2

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Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNGMKILPGLYIGNPKDAADAPQLSKNKVTHLSVHDSARPMLGVKVCIPAAADSPS 60
Db 1 MGNGMKILPGLYIGNPKDAADAPQLSKNKVTHLSVHDSARPMLGVKVCIPAAADSPS 60
Qy 61 QNLTTRHFKESIKFTHCRLRGESCLVHCLAGSVSVTLVIAYIMTVTDFGVEDALHTVRA 120
Db 61 QNLTTRHFKESIKFTHCRLRGESCLVHCLAGSVSVTLVIAYIMTVTDFGVEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQEFKEHVHQYRQLKEEYGESPLQDAEEAKNLAAPGILKFWAF 180

Db 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 2
US-10-264-237-2811
; Sequence 2811, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264.237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2811
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2811

Query Match 100.0%; Score 975; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60
Db 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60
Qy 61 QNLTRHPKESIKFTIHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTRHPKESIKFTIHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 3
US-10-072-012-698
; Sequence 428, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A

; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Riéger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072.012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 428
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-428
Query Match 100.0%; Score 975; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60
Db 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60
Qy 61 QNLTRHPKESIKFTIHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTRHPKESIKFTIHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184
RESULT 4
US-10-072-012-696
; Sequence 696, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara

APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 696
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-696

Query Match 100.0%; Score 975; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 60
Db 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 60
Qy 61 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 5
US-10-444-795B-779
Sequence 779, Application US/10444795B
Publication No. US20040077574A1

GENERAL INFORMATION:
APPLICANT: Klinghoffer, Richard
APPLICANT: Lewis, Stephen Patrick
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
FILE REFERENCE: 200125.449
CURRENT APPLICATION NUMBER: US/10/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 779
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-444-795B-779

Query Match 100.0%; Score 975; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 60
Db 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 60
Qy 61 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 6
US-10-103-313-395
Sequence 395, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: RJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 395
LENGTH: 190
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-313-395

Query Match 100.0%; Score 975; DB 14; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 60
Db 7 MGNMKNILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPAADS 66
Qy 61 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db 67 QNLTRHFKESIKFTHICRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 126
Qy 121 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180
Db 127 GRSCANPNVGFQRLQEFKEHVEHYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 186
Qy 181 LRRL 184

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Db          187 LRRL 190
|||||
RESULT 7
US-10-103-313-523
; Sequence 523, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 523
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-523

Query Match      100.0%; Score 975; DB 14; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 1 MGNGMKILPGLYIGNFKDARDASQLSKNVTHTLSVHDSARPMLGVKYLICIPAADSPS 60
Db 7 1 MGNGMKILPGLYIGNFKDARDASQLSKNVTHTLSVHDSARPMLGVKYLICIPAADSPS 66

Qy 61 QNLTTRHPKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 67 QNLTTRHPKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 126

Qy 121 GRSCAMPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 127 GRSCAMPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 186

Qy 181 LRRL 184
|||||
RESULT 8
US-10-151-320-15
; Sequence 15, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436
; CURRENT APPLICATION NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-320-15

Query Match      98.4%; Score 959; DB 14; Length 184;
Best Local Similarity 98.9%; Pred. No. 1.5e-97;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 1 MGNGMKILPGLYIGNFKDARDASQLSKNVTHTLSVHDSARPMLGVKYLICIPAADSPS 60
Db 1 1 MGNGMKILPGLYIGNFKDARDASQLSKNVTHTLSVHDSARPMLGVKYLICIPAADSPS 60

Qy 61 QNLTTRHPKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120

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Best Local Similarity 93.5%; Pred. No. 1.4e-94;
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNGMKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLICIPAADSPS 60
Db 1 MGSGMSQILPGLYIGNFKDARDAEQLSKNKVTHLSVHDTARPMLGVKYLICIPAADTPS 60

Qy 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQROLOEFKEHVEHGYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNLGFQROLOEFKEHVEHGYRQWLKEEYGENPLRDAEAKNLAAPGILKYWAF 180

Qy 181 LRLR 184
Db 181 LRLR 184

RESULT 10
US-10-072-012-697
; Sequence 697, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 697
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-072-012-697

Query Match 95.6%; Score 932; DB 15; Length 184;
Best Local Similarity 93.5%; Pred. No. 1.4e-94;
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNGMKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLICIPAADSPS 60
Db 1 MGSGMSQILPGLYIGNFKDARDAEQLSKNKVTHLSVHDTARPMLGVKYLICIPAADTPS 60

Qy 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQROLOEFKEHVEHGYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNLGFQROLOEFKEHVEHGYRQWLKEEYGENPLRDAEAKNLAAPGILKYWAF 180

Qy 181 LRLR 184
Db 181 LRLR 184

RESULT 11
US-10-072-012-430
; Sequence 430, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02

NPA

NPA

; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (40)..(46)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-072-012-430

Query Match 94.7%; Score 923; DB 15; Length 184;
Best Local Similarity 94.6%; Pred. No. 1.4e-93;
Matches 174; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPADSPS 60
Db 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPADSPS 60

Qy 61 QNLTFRHFKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTFRHFKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 12
US-10-072-012-698
; Sequence 698, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012

NPA

; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 698
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (40)..(46)
; OTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-072-012-698

Query Match 94.7%; Score 923; DB 15; Length 184;
Best Local Similarity 94.6%; Pred. No. 1.4e-93;
Matches 174; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPADSPS 60
Db 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPADSPS 60

Qy 61 QNLTFRHFKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 QNLTFRHFKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 13
US-10-803-738-2
; Sequence 2, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
; APPLICANT: Belmont, John
; APPLICANT: Fletcher, Frederick
; APPLICANT: Chen, Alice
; APPLICANT: Jurecic, Roland
; APPLICANT: Colicos, Suzanne
; APPLICANT: Tan, Tse-Hua
; APPLICANT: Zhou, Guisheng
; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
; FILE REFERENCE: 99-383-B
; CURRENT APPLICATION NUMBER: US/10/803,738
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/665,819A
; PRIOR FILING DATE: 2000-09-20

;; PRIOR APPLICATION NUMBER: US 60/155,068
;; PRIOR FILING DATE: 1999-09-21
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 205
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-803-738-2

Query Match 92.0%; Score 897; DB 17; Length 205;
Best Local Similarity 90.5%; Pred. No. 1.2e-90;
Matches 172; Conservative 3; Mismatches 5; Indels 10; Gaps 1;
Qy 1 MGNMKNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTS 60
Db 1 MGNMKNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTS 60
Qy 61 QNLTRHFKEKIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120
Db 61 QNLTRHFKEKIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQOEPEKHEVHOYRQWLKEEYGESPLQDAEEAKNITLA----- 170
Db 121 GRSCANPNVGFQRLQOEPEKHEVHOYRQWLKEEYGESPLQDAEEAKNITLA----- 170
Qy 171 APGILKFWAF 180
Db 181 QGARRWSSP 190

RESULT 14

US-10-803-738-4
;; Sequence 4, Application US/10803738
;; Publication No. US20050014222A1
;; GENERAL INFORMATION:
;; APPLICANT: Belmont, John
;; APPLICANT: Fletcher, Frederick
;; APPLICANT: Chen, Alice
;; APPLICANT: Jurecic, Roland
;; APPLICANT: Colicos, Suzanne
;; APPLICANT: Tan, Tse-Hua
;; APPLICANT: Zhou, Guisheng
;; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
;; FILE REFERENCE: 99-383-B
;; CURRENT APPLICATION NUMBER: US/10/803,738
;; CURRENT FILING DATE: 2004-03-18
;; PRIOR APPLICATION NUMBER: US/09/665,819A
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: US 60/155,068
;; PRIOR FILING DATE: 1999-09-21
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4
;; LENGTH: 205
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-803-738-4

Query Match 86.5%; Score 843; DB 17; Length 205;
Best Local Similarity 92.3%; Pred. No. 1.2e-84;
Matches 156; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGNMKNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTS 60
Db 1 MGNMKNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTS 60
Qy 61 QNLTRHFKEKIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120
Db 61 QNLTRHFKEKIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120
Qy 121 GRSCANPNVGFQRLQOEPEKHEVHOYRQWLKEEYGESPLQDAEEAKNITL 169
Db 121 GRSCANPNVGFQRLQOEPEKHEVHOYRQWLKEEYGESPLQDAEEAKNITL 169

Db 121 GRSCANPNLGFQRLQOEPEKHEVHOYRQWLKEEYGENPLRDAEEAKNITL 169

RESULT 15

US-10-803-738-5
;; Sequence 5, Application US/10803738
;; Publication No. US20050014222A1
;; GENERAL INFORMATION:
;; APPLICANT: Belmont, John
;; APPLICANT: Fletcher, Frederick
;; APPLICANT: Chen, Alice
;; APPLICANT: Jurecic, Roland
;; APPLICANT: Colicos, Suzanne
;; APPLICANT: Tan, Tse-Hua
;; APPLICANT: Zhou, Guisheng
;; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways
;; FILE REFERENCE: 99-383-B
;; CURRENT APPLICATION NUMBER: US/10/803,738
;; CURRENT FILING DATE: 2004-03-18
;; PRIOR APPLICATION NUMBER: US/09/665,819A
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: US 60/155,068
;; PRIOR FILING DATE: 1999-09-21
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 5
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: mJKAP
US-10-803-738-5

Query Match 70.8%; Score 690; DB 17; Length 138;
Best Local Similarity 93.5%; Pred. No. 5.9e-68;
Matches 129; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Qy 5 MNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTSQNL 64
Db 1 MSQILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADSPTSQNL 60
Qy 65 RHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRAGRSC 124
Db 61 RHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRAGRSC 120
Qy 125 ANPNVGFQRLQOEPEKHE 142
Db 121 ANPNVGFQRLQOEPEKHE 138

Search completed: July 21, 2005, 19:26:24
Job time : 72 secs

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